

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: July 7, 2005, 12:36:09 ; Search time 42 Seconds
(without alignments)
1184.383 Million cell updates/sec

Title: US-10-618-173-2
Perfect score: 2712
Sequence: 1 MMSRDTKTESQSQSGTSSSS.....ASTSSCSILPTSAEKRAKR 517

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	621	22.9	513	1 S43941	protein kinase DUN
2	593.5	21.9	374	1 S50193	Ca2+/calmodulin-de
3	591.5	21.8	370	1 S57347	Ca2+/calmodulin-de
4	575.5	21.2	821	1 A39616	protein kinase RAD
5	563.5	20.8	460	2 S58882	protein kinase Cds
6	560.5	20.7	301	1 A40811	myosin-light-chain
7	539.5	19.9	469	1 S17656	Ca2+/calmodulin-de
8	538	19.8	445	2 T43420	probable protein k
9	537	19.8	348	2 T37321	Ca2+/calmodulin-de
10	535	19.7	524	2 A45472	protein kinase (EC
11	534.5	19.7	474	1 TVRTCA	Ca2+/calmodulin-de
12	534.5	19.7	502	2 I52637	Ca2+/calmodulin-de
13	531	19.6	473	1 A53036	Ca2+/calmodulin-de
14	507.5	18.7	735	2 A53300	ribosomal protein
15	506	18.7	560	2 S51600	phosphorylase kina
16	503.5	18.6	735	2 I51901	ribosomal protein
17	501.5	18.5	414	2 JN0323	Ca2+/calmodulin-de
18	501.5	18.5	504	2 T10449	probable serine/th
19	501	18.5	512	1 JC1446	serine/threonine-s
20	498.5	18.4	724	1 B32571	ribosomal protein
21	498	18.4	608	2 T18445	hypothetical prote
22	494.5	18.2	516	1 JU0270	Ca2+/calmodulin-de
23	493.5	18.2	509	2 B44412	calmodulin-depende
24	493.5	18.2	530	2 D44412	Ca2+/calmodulin-de
25	492.5	18.2	473	1 S59941	serine/threonine-s
26	490	18.1	511	1 A56009	serine/threonine-s
27	488	18.0	512	2 T52633	serine/threonine-s
28	487	18.0	504	2 T38226	probable serine-th
29	484.5	17.9	542	2 T08777	probable protein k

30	484	17.8	918	1 I48719	protein kinase C (
31	480.5	17.7	310	2 B88640	protein K07A9.2 (i
32	479.5	17.7	518	1 B46619	Ca2+/calmodulin-de
33	479.5	17.7	518	1 S43845	Ca2+/calmodulin-de
34	479.5	17.7	527	1 A31908	Ca2+/calmodulin-de
35	479.5	17.7	556	2 JC5636	Ca2+/calmodulin-de
36	479	17.7	912	1 A53215	protein kinase C (
37	478.5	17.6	533	1 A34366	Ca2+/calmodulin-de
38	478.5	17.6	580	2 T40939	probable Ca-calmod
39	473.5	17.5	520	2 F85059	probable calcium d
40	471.5	17.4	512	2 T07788	probable serine/th
41	470.5	17.3	503	2 T51156	calcium dependent
42	470.5	17.3	752	1 A32571	ribosomal protein
43	469	17.3	472	2 B90100	SNF-related kinase
44	469	17.3	490	1 S71776	calcium-dependent
45	468	17.3	1142	2 S59359	GIN4 protein - yea

ALIGNMENTS

RESULT 1

S43941
protein kinase DUN1 (EC 2.7.1.1) - Yeast (Saccharomyces cerevisiae)
N:Alternate names: protein D2370; protein YDL101c
C:Species: Saccharomyces cerevisiae
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S43941; S67643; S67418; S72106
R:Zhou, Z.; Ellledge, S.J.
Cell 75, 1119-1127, 1993
A:Title: DUN1 encodes a protein kinase that controls the DNA damage response in yeast.
A:Reference number: S43941; MUID:94084787; PMID:8261511
A:Accession: S43941
A:Molecule type: DNA
A:Residues: 1-513 <ZHO>
A:Cross-references: UNIPROT:P39009; EMBL:L25548; NID:G435616; PIDN:AAA16324.1; PID:G43561
R:Ballesta, J.P.G.; Ramacha, M.; Soler-Mira, A.; Jimenez, A.; Garcia-Cantalejo, J.M.; Bo
submitted to the Protein Sequence Database, July 1996
A:Reference number: S67629
A:Accession: S67643
A:Molecule type: DNA
A:Residues: 1-513 <BAL>
A:Cross-references: EMBL:Z74149; NID:G1431139; PIDN:CAA98668.1; PID:G1431140; GSPDB:GNO0
A:Experimental source: Strain S288C
R:Bozkovic, J.; Saiz, J.E.; Soler-Mira, A.; Garcia-Cantalejo, J.; Revuelta, J.L.; Jimine
submitted to the EMBL Data Library, February 1996
A:Reference number: S67406
A:Accession: S67418
A:Molecule type: DNA
A:Residues: 1-513 <BOS>
A:Cross-references: EMBL:X95644; NID:G1199535; PIDN:CAA64912.1; PID:G1199548
R:Saiz, J.E.; Buitrago, M.J.; Garcia, R.; Revuelta, J.L.; del Rey, F.
Yeast 12, 1077-1084, 1996
A:Title: The sequence of a 20.3 kb DNA fragment from the left arm of Saccharomyces cerevi
A:Reference number: S72094; MUID:97051597; PMID:8896274
A:Accession: S72106
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-513 <SAI>
A:Cross-references: EMBL:X95644; NID:G1199535; PIDN:CAA64912.1; PID:G1199548
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996
C:Genetics:
A:Gene: SGD:DUN1; MIPS:YDL101c
A:Cross-references: MIPS:YDL101c; SGD:S0002259
A:Map position: 4L
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
C:Superfamily: protein kinase DUN1; kinase interaction domain homology; protein kinase h
C:Keywords: ATP; nucleus; phosphoprotein; phosphotransferase; serine/threonine-specific k
F:58-128/Domain: kinase interaction domain homology <KIH>
F:198-480/Domain: protein kinase homology <KIN>
F:206-214/Region: protein kinase ATP-binding motif

A;Title: S-phase specific activation of Cds1 kinase defines a subpathway of the checkpoint
A;Reference number: Z26084; MUID:98119835; PMID:9450932
A;Accession: T52473
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-202, 'I', 204-237, 'F', 239-460 <LIN>
A;Cross-references: EMBL:A0222869; NID:g2689196; PIDN:CAAL1019.1; PID:g2689197
C;Genetics:
A;Gene: SPBC1885.11C; cds1
A;Map position: 3
A;Introns: 86/3; 103/1; 113/3; 142/1; 228/3; 298/3; 368/2
C;Function:
A;Description: EC 2.7.1.-; protein kinase Cds1 [validated, MUID:98119835]; is required for S-phase arrest and activated by S-phase arrest and activated by DNA damage
A;Note: Cds1 is phosphorylated and activated by S-phase arrest and activated by DNA damage
C;Superfamily: protein kinase Cds1; kinase interaction domain homology; protein kinase H
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F;62-133/Domain: kinase interaction domain homology <KIN>
F;165-433/Domain: protein kinase homology <KIN>
F;173-181/Region: protein kinase ATP-binding motif
Query Match 20.8%; Score 563.5; DB 2; Length 460;
Best Local Similarity 33.3%; Pred. No. 7.8e-19;
Matches 144; Conservative 75; Mismatches 163; Indels 51; Gaps 13;
QY 87 FGRDKCDYTFDIPVLNQTDRYKTSKRHRIFQELHGH-----SRVANIEDLSNGTFF 141
DB 62 FGRHKSCEVLNCP-----RVSNPFHFYIQ--GHRNDSDESENVVFLHDHSSNGTFF 110
QY 142 VNKEIIGKRTIPLTNAAE--TALSPTNKVFVSDLSV-----DQTYPKDFIDKYIMS 195
DB 111 LNFERLAKNSRTLNSGDBIRIGLGVPKDEISFLCQVPVHKSRDSQKNMKSENSHYEII 170
QY 196 RPIGSGACGEVKLAFQSKVCKVAVKIIKSRKFKMNTSSNEHPISVDTEIETILKLDHPC 255
DB 171 RILSGSTFAVKLAVENVSKGKVAIKINRKLITSEKRATEFQREIDILKSLHHPG 230
QY 256 IIKIENFFDSDFYIVLELMEGGELFDRVNVSTRLEPIAKLYFYQMLLAVQYLHENG 315
DB 231 VVQCHEICNDDELFIWVEYEGDLMDFLIANGSIDQCKPFLKQLLETLLHLHKGV 290
QY 316 IHRDLKPNVLSSSECCIKITDFGQSKIL-GETSLMRTLCTGPTTYLAVPELVNTAGTT 374
DB 291 THRDLKPNELITN--DFHLKISDFGLAKVTHGTFTLETFCGFMGLAVPELVLSKNVN 347
QY 375 ---GYSSAVDCWSGLVILFVCLCGYPPF--SQNSNIPLNKQIARGKTYTIAAARNVSE 429
DB 348 LDGGYDDKVDIWSLGCVLVYMLTASIPFASSQAKCIEL---ISKGATPIEPLENEISE 404
QY 430 QAFDLVKNLLVVDPEQRLTTKQALEHPMLQDDSMKHTVERLMYGVDMTPPPPIKKNIRK 489
DB 405 EGIDILNRMLEINPEKRISSEALQHPWF-----YTVST---HEHRTPPSSSE----- 449
QY 490 RGHWDQDASTSS 502
DB 450 --HEATEQLNSSS 460
RESULT 6
A40811
N;Title: myosin-light-chain kinase (EC 2.7.1.117) A - slime mold (Dictyostelium discoideum)
N;Alternate names: MLCK-A
C;Species: Dictyostelium discoideum
C;Date: 10-Apr-1992 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004
C;Accession: A40811; A37125
R;Tan, J.L.; Spudich, J.A.
J. Biol. Chem. 266, 16044-16049, 1991
A;Title: Characterization and bacterial expression of the Dictyostelium myosin light chain
A;Reference number: A40811; MUID:91340753; PMID:1651931
A;Accession: A40811
A;Molecule type: mRNA
A;Residues: 1-301 <TAN>
A;Cross-references: UNIPROT:P25323; GB:M64176; NID:gl498249; PIDN:AAB06337.1; PID:gl498249
R;Tan, J.L.; Spudich, J.A.

J. Biol. Chem. 265, 13818-13824, 1990
A;Title: Dictyostelium myosin light chain kinase. Purification and characterization.
A;Reference number: A37125; MUID:90337997; PMID:2380188
A;Accession: A37125
A;Molecule type: protein
A;Residues: 9-12, 'I', 14-19; 163-167, 'S', 169-179; 192-198 <TA2>
C;Genetics:
A;Gene: mlka
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine in itself
A;Pathway: cytokinesis; fruiting body formation
A;Note: not activated by Ca2+/calmodulin in contrast with MLCK from higher eukaryotes
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; autophosphorylation; cell division; phosphoprotein; phosphotransferase;
F;6-265/Domain: protein kinase homology <KIN>
F;14-22/Region: protein kinase ATP-binding motif
F;1267-295/Domain: inhibitory #status predicted <INH>
F;37/Active site: Lys #status predicted
F;296/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicted
Query Match 20.7%; Score 560.5; DB 1; Length 301;
Best Local Similarity 38.7%; Pred. No. 7.1e-19;
Matches 116; Conservative 58; Mismatches 105; Indels 21; Gaps 5;
QY 192 YIMSRPIGSGACGEVKLAFQSKVCKVAVKIIKSRKFKMNTSSNEHPISVDTEIETILK 251
DB 8 YEFKEELGRGAFSIVYIGENKQTKQRYAIVKINSELGKDYEK-----LKNVEDILKKV 62
QY 252 DHPCHIKIENFFDSDFYIVLELMEGGELFDRVNVSTRLEPIAKLYFYQMLLAVQYLH 311
DB 63 NHPNIIALKELFDTPKLYLVMELVTGGLFDKIVKGVSEADAANLVKKIVSAVGYLH 122
QY 312 ENGVIHRDLKPNVLSSSECCIKITDFGQSKILGETSLMRTLCTGPTTYLAVPELVNTA 371
DB 123 GLNTVHRDLKPNVLSSSECCIKITDFGQSKILGETSLMRTLCTGPTTYLAVPELVN-- 180
QY 372 GTTCYSSAVDCWSGLVILFVCLCGYPPFSEQNSNIP-LKNQIARGKTYTIAAARNVSEQ 430
DB 181 -ATGYDEKVDMSIGVITYILLCCGFPF--YGDVIFEIFEIQMEVNFPEYFEGGTSKE 237
QY 431 AFDLVKNLLVVDPEQRLTTKQALEHPMLQDDSMKHTVERLMYGVDMTPPPPIKKNIRK 490
DB 238 AKDFIGKLLVVDVSKRLNATNALNHPMLKSNNSNTIDTV-----KMKYEVIVERR 287
RESULT 7
S17656
Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) IV - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S17656; A29878; I49571
R;Jones, D.A.; Glod, J.; Wilson-Shaw, D.; Hahn, W.E.; Sikela, J.M.
FEBS Lett. 289, 105-109, 1991
A;Title: cDNA sequence and differential expression of the mouse Ca(2+)/calmodulin-dependent protein kinase II
A;Reference number: S17656; MUID:91372388; PMID:1893997
A;Accession: S17656
A;Molecule type: mRNA
A;Residues: 1-469 <JON>
A;Cross-references: UNIPROT:P08414; EMBL:X58995; NID:g50366; PIDN:CAA41741.1; PID:g50367
R;Sikela, J.M.; Hahn, W.E.
Proc. Natl. Acad. Sci. U.S.A. 84, 3038-3042, 1987
A;Title: Screening an expression library with a ligand probe: isolation and sequence of a cDNA
A;Reference number: A29878; MUID:87204263; PMID:3033675
A;Accession: A29878
A;Molecule type: mRNA
A;Residues: 315-469 <SIK>
A;Cross-references: GB:M16206; NID:g200360; PIDN:AAA39933.1; PID:g387512
R;Sikela, J.M.; Law, M.L.; Kao, F.
Genomics 4, 21-27, 1989
A;Title: Chromosomal localization of the human gene for brain Ca2+/calmodulin-dependent protein kinase II
A;Reference number: I49571; MUID:89122027; PMID:2536634
A;Accession: I49571

QY 429 EQAFDLVKNLLVDPPEORLTTKQALEHPWLODDSMKHTVERLMYGVDDHTMPPPIKNIIR 488
Db 249 GSAKDFTHLMCCDPEARFTQDALSHPWISGNT-----AYTHDIGTIVAVHLKSLAK 302
QY 489 K 489
Db 303 R 303

RESULT 10
A45472
protein kinase (EC 2.7.1.37) - malaria parasite (Plasmodium falciparum)
N;Alternate names: calcium-dependant protein kinase
C;Species: Plasmodium falciparum
C;Date: 17-Feb-1994 #sequence revision 17-Feb-1994 #text_change 09-Jul-2004
C;Accession: A45472; E71605; S28590
R;Zhao, Y.; Kappes, B.; Franklin, R.M.
J. Biol. Chem. 268, 4347-4354, 1993
A;Title: Gene structure and expression of an unusual protein kinase from Plasmodium falciparum
A;Reference number: A45472; MUID:93179444; PMID:8440720
A;Contents: K1
A;Accession: A45472
A;Molecule type: DNA
A;Residues: 1-524 <ZHA>
A;Cross-references: UNIPROT:Q27731; EMBL:X67288; NID:g9877; PIDN:CAA47704.1; PID:g9878
A;Note: sequence extracted from NCBI backbone (NCBIN:125849, NCBI:125850)
R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;
; Pertera, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.
Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A;Reference number: A71600; MUID:99021743; PMID:9804551
A;Accession: E71605
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-524 <GAR>
A;Cross-references: GB:AE001419; GB:AE001362; NID:g3845281; PIDN:AAC71952.1; PID:g3845282
A;Experimental source: clone 3D7
C;Genetics:
A;Gene: cpk; PFB0815w
A;Introns: 406/3; 440/1; 479/3; 505/3
C;Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kinase
C;Keywords: ATP; calcium binding; EF hand; phosphotransferase; serine/threonine-specific
F;54-325/Domain: protein kinase homology <KIN>
F;62-70/Region: protein kinase ATP-binding motif
F;416-448/Domain: calmodulin repeat homology <EF4>

Query Match 19.7%; Score 535; DB 2; Length 524;
Best Local Similarity 35.3%; Pred. No. 1.7e-17;
Matches 124; Conservative 60; Mismatches 125; Indels 42; Gaps 7;
QY 125 GHSRVANIEDLSNGTGVFNKEIIGKGTPLTNNAEIALSLPTNNAEIALSLPTNNKVFVPSDLSDVDDTIY 184
Db 2 GCSSQSNVKDF-----KTRSRFTNGNNYKGS-GNNK-----NSEDALIN 40
QY 185 PKDFIDK-----YIMSRPIGSGAGEVKLAFQKSVCKKVAVKIISKKKFKMMNTSSNE 236
Db 41 PGMVVRKEGKIGESYFKVRKLGSGAGEVLLCRKHGCHGEKAIKIKSQDFPMKYISIT 100
QY 237 HPTISVD-----TEIILKLDHPICIIKENFFOSDFYIIVLELMGEGGLFDRVWNS 288
Db 101 NKIECDKDHIEEYNEISLLKSLDHPNI IKLFQVFEKDYFYLVTPEYEGGELFEQIINR 160
QY 289 TRLREPTAKLYFQMLLAVOYLHENGVIHDLKPNVLLSSTSECCIKITDFGQSKILG 348
Db 161 HKFDECDAAIMKQILSGICYLHKHNHVRDIKPENILLNKHSLNLIKIVDFGLSFFS 220
QY 349 ETSIMRLTLCGPTYLAPEVLNLTAGTTCYSSAVDCWSLGVILFVCLCGYPPFSQNSNIP 408
Db 221 KDNKLDRLGTAYIAPEVLKK-----YNEKCDWWSGVILYLLCGYPPFGQNDQDII 276
QY 409 KNQIAEGKYTYIAAANRWNSQAFDLVKNLLVDPPEORLTTKQALEHPWLODDSMKHTVERLMYGVDDHTMPPPIKNIIR 488

Db 277 K-KVEKGKVFDFNDWKNISEAEKLIKMLTYDYNKRITAKEALNSKWIK 326

RESULT 11

TVRTC4

Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) IV - rat

N;Alternate names: Ca2+/calmodulin-dependent protein kinase Gr

N;Contains: calipermin

C;Species: Rattus norvegicus (Norway rat)

C;Date: 31-Mar-1993 Nucleotide revision 31-Mar-1993 #text change 09-Jul-2004

C;Accession: A41103; A41237; A32865; A41250; A32035; A60255; I53706

R;Ohmstede, C.A.; Bland, M.M.; Merril, B.M.; Sahyoun, N.

Proc. Natl. Acad. Sci. U.S.A. 88, 5784-5788, 1991

A;Title: Relationship of genes encoding Ca(2+)/calmodulin-dependent protein kinase Gr and

A;Reference number: A41103; MUID:91288548; PMID:1648230

A;Accession: A41103

A;Molecule type: DNA

A;Residues: 47-141, 'NE', 144-474 <OH1>

A;Cross-references: UNIPROT:P13234; GB:M74488; NID:G203219; PIDN:AAA40845.1; PID:G2032220

A;Note: This sequence has been revised in reference A41237

A;Note: part of this sequence was confirmed by sequencing of cDNA to mRNA

R;Ohmstede, C.A.; Bland, M.M.; Merril, B.M.; Sahyoun, N.

Proc. Natl. Acad. Sci. U.S.A. 88, 9375, 1991

A;Reference number: A41237

A;Accession: A41237

A;Molecule type: DNA

A;Residues: 142-143 <OH2>

A;Cross-references: GB:M63334

A;Note: This is a revision to the sequence from reference A41103

R;Ohmstede, C.A.; Jensen, K.F.; Sahyoun, N.E.

J. Biol. Chem. 264, 5866-5875, 1989

A;Title: Ca(2+)/calmodulin-dependent protein kinase enriched in cerebellar granule cells

A;Reference number: A32865; MUID:89174647; PMID:2538431

A;Accession: A32865

A;Molecule type: mRNA

A;Residues: 250-474 <OH3>

A;Cross-references: GB:J04600; NID:G206172; PIDN:AAA41867.1; PID:G206173

R;Means, A.R.; Cruzalegui, F.; LeMaugeres, B.; Needleman, D.S.; Slaughter, G.R.; Ono, T.

Mol. Cell. Biol. 11, 3960-3971, 1991

A;Title: A novel Ca(2+)/calmodulin-dependent protein kinase and a male germ cell-specific

A;Reference number: A41250; MUID:91304387; PMID:1649385

A;Accession: A41250

A;Molecule type: mRNA

A;Residues: 1-371, 'M', 373-408, 'Q', 410-474 <MEA>

A;Cross-references: GB:M64757

R;Ono, T.; Slaughter, G.R.; Cook, R.G.; Means, A.R.

J. Biol. Chem. 264, 2081-2087, 1989

A;Title: Molecular cloning sequence and distribution of rat calpermin, a high affinity c

A;Reference number: A32035; MUID:89123272; PMID:2914893

A;Accession: A32035

A;Molecule type: mRNA

A;Residues: 306-371, 'M', 373-474 <ON1>

A;Cross-references: GB:J04446; NID:G203642; PIDN:AAA40990.1; PID:G203643

R;Ono, T.; Means, A.R.

Adv. Exp. Med. Biol. 255, 263-268, 1989

A;Title: Calpermin is a testis specific calmodulin-binding protein closely related to Ca

A;Reference number: A60255; MUID:90144189; PMID:2618865

A;Accession: A60255

A;Molecule type: protein

A;Residues: 335-363 <ON2>

A;Note: the amino end of calpermin was blocked

R;Bland, M.M.

Gene 137, 351-352, 1993

A;Title: Identification of alternate 5' untranslated regions in the gene encoding Ca2+/cal

A;Reference number: I53706; MUID:94131312; PMID:8299971

A;Accession: I53706

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-37 <RES>

A;Cross-references: GB:L16999; NID:G310086; PIDN:AAA17443.1; PID:G310087

C;Comment: Ca2+/calmodulin-dependent protein kinase IV is enriched in cerebellar granule

and in sperm cells.

C;Superfamily: Ca2+/calmodulin-dependent protein kinase; protein kinase homology

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OM protein - protein search, using sw model

Run on: July 7, 2005, 12:34:23 ; Search time 178 Seconds
(without alignments)
1487.331 Million cell updates/sec

Title: US-10-618-173-2

Perfect score: 2712

Sequence: 1 MMSRDTKTESQSQSGTSSSS.....ASTSSCEILPTSAEKRAKR 517

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 03.*

1: uniprot_prot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2712	100.0	517	Q918V3	Q918V3 xenopus lae
2	2704	99.7	517	Q98TW0	Q98TW0 xenopus lae
3	1655.5	61.0	543	1 CHK2_HUMAN	Q96017 homo sapien
4	1644.5	60.6	545	2 Q9R019	Q9R019 rattus norv
5	1637	60.4	546	1 CHK2_MOUSE	Q92265 mus musculu
6	1624	59.9	586	2 Q6QA11	Q6QA11 homo sapien
7	1499	55.3	514	2 Q9HCQ8	Q9HCQ8 homo sapien
8	1317.5	48.6	503	2 Q90Z15	Q90Z15 brachydanio
9	1311.5	48.4	503	2 Q803E2	Q803E2 brachydanio
10	1287	47.5	452	2 Q6QA05	Q6QA05 homo sapien
11	1066	39.3	322	2 Q9HBS5	Q9HBS5 homo sapien
12	1012.5	37.3	339	2 Q6QA08	Q6QA08 homo sapien
13	828	30.5	476	1 LOK_DROME	Q61267 drosophila
14	791	29.2	289	2 Q6QA10	Q6QA10 homo sapien
15	727.5	26.8	712	2 Q7SEK0	Q7SEK0 neurospora
16	644.5	23.8	443	2 Q6BH59	Q6BH59 debaryomyce
17	621.5	22.9	476	1 CHK2_CAEEL	Q9HLY5 caenorhabdi
18	621	22.9	513	1 DUNI_YEAST	Q39009 saccharomyc
19	619.5	22.8	506	2 Q6FKZ8	Q6FKZ8 candida gla
20	610.5	22.5	378	2 Q8AVN4	Q8AVN4 xenopus lae
21	605	22.3	472	2 Q9XTX3	Q9XTX3 caenorhabdi
22	603	22.2	469	2 Q9HBS5	Q9HBS5 homo sapien
23	602.5	22.2	388	2 Q64HW3	Q64HW3 oncorhynch
24	600.5	22.1	357	2 Q9HD31	Q9HD31 homo sapien
25	600.5	22.1	367	2 Q8BW17	Q8BW17 mus musculu
26	600.5	22.1	385	2 Q8IU85	Q8IU85 homo sapien
27	600.5	22.1	385	2 Q8BW96	Q8BW96 mus musculu
28	599.5	22.1	382	2 Q8AYR2	Q8AYR2 xenopus lae
29	595.5	22.0	377	2 Q8OW64	Q8OW64 mus musculu
30	595.5	22.0	415	2 Q6CPX0	Q6CPX0 kluyveromyc
31	593.5	21.9	374	1 KCCL_MOUSE	Q91Y88 mus musculu

ALIGNMENTS

RESULT 1

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Q918V3
ID Q918V3 PRELIMINARY; PRT; 517 AA.
AC Q918V3;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DE 01-OCT-2003 (Tremblrel. 25, Last annotation update)
GN Name=Cds1;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20255216; PubMed=10793133;
RA Guo Z., Dunphy W.G.;
RT "Response of Xenopus Cds1 in cell-free extracts to DNA templates with
double-stranded ends."
RL Mol. Biol. Cell 11:1535-1546(2000).
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AF174295; AAF75829.1; -.
DR HSSP; Q96017; IGXC.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000253; FHA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR008984; SMAD_FHA.
DR Pfam; PF00498; FHA; 1.
DR Pfam; PF00669; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00240; FHA; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS50006; FHA DOMAIN; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 517 AA; 58261 MW; 39DC05689090DB19 CRC64;
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Query Match 100.0%; Score 2712; DB 2; Length 517;

Best Local Similarity 100.0%; Pred. No. 1.4e-164; Indels 0; Gaps 0;

Matches 517; Conservative 0; Mismatches 0;

QY 1 MMSRDTKTESQSQSGTSSSSSSAPQSYSSQSSSGTSLSLDTPVPQDLASIFDEPDEID 60

Db 1 MMSRDTKTESQSQSGTSSSSSSAPQSYSSQSSSGTSLSLDTPVPQDLASIFDEPDEID 60

QY 61 IPQPWGRWLWALGKGFNLHNDLHEEVFGDRDKCDYTFDIPVLNQTRDYKTSKRHFRIQ 120

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Db 61 IPQWGRWALGKGFNLHDCLEHEEVFGKDKCDYTFDIPVLNQTDYKTSKRHFRIQ 120
Qy 121 ELGHGHSRVANIEDLSNGTGFVNKEIIGKGRTPLTNNAEIALSLPTNKVFVFSLSVDD 180
Db 121 ELGHGHSRVANIEDLSNGTGFVNKEIIGKGRTPLTNNAEIALSLPTNKVFVFSLSVDD 180
Qy 181 QTIYPKDFIDKYIMSRPIGSGACGEVKLAFQSVCKVAVKIIISKRKFMTSSNEHPIS 240
Db 181 QTIYPKDFIDKYIMSRPIGSGACGEVKLAFQSVCKVAVKIIISKRKFMTSSNEHPIS 240
Qy 241 VDTETIILKLDHPICIIKIENPFDEDFYIIVLELMEGGEPLFDRVNVNSTRLEPIAKLYF 300
Db 241 VDTETIILKLDHPICIIKIENPFDEDFYIIVLELMEGGEPLFDRVNVNSTRLEPIAKLYF 300
Qy 301 YQMLLAQVYLHENGVIHRDLKPEVLLSTSECCIKITDFGQSKILGETSLMRTLCTGP 360
Db 301 YQMLLAQVYLHENGVIHRDLKPEVLLSTSECCIKITDFGQSKILGETSLMRTLCTGP 360
Qy 361 TYLAPEVLNTAGTTGYSSAVDCWSLGVILFVCLCGYPPFSEQNSIPLKNQIAEGKYTYI 420
Db 361 TYLAPEVLNTAGTTGYSSAVDCWSLGVILFVCLCGYPPFSEQNSIPLKNQIAEGKYTYI 420
Qy 421 AAARNVSEQAPDLVKNLLVVDPEQRLTTKQALEHPWLQDDSMKHTVERLMYGVVDHTWPP 480
Db 421 AAARNVSEQAPDLVKNLLVVDPEQRLTTKQALEHPWLQDDSMKHTVERLMYGVVDHTWPP 480
Qy 481 PIKKNIIIRKRGHEWDQDASTSSCSSEILPTSAEKRAKR 517
Db 481 PIKKNIIIRKRGHEWDQDASTSSCSSEILPTSAEKRAKR 517
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RESULT 2

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Q98TW0 PRELIMINARY; PRT; 517 AA.
ID Q98TW0
AC Q98TW0;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Protein kinase Cds1.
GN Name=Cds1;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]_TaxID=8355;
RP SEQUENCE FROM N.A.
RA Matsui T., Nakanishi M., Takisawa H.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL: AF326574; AG59884.1; -.
DR HSSP: Q96017; LGXC.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR000253; FHA.
DR InterPro: IPR011009; Kinase_like.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR InterPro: IPR008271; Ser_thr_pkin_AS.
DR InterPro: IPR008984; SMAD_FHA.
DR Pfam: PF00498; FHA; 1.
DR Pfam: PF00699; Pkinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00240; FHA; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS50006; FHA_DOMAIN; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 517 AA; 58310 MW; 401A3235AA0BDCBE CRC64;
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Query Match 99.7%; Score 2704; DB 2; Length 517;
Best Local Similarity 99.8%; Pred. No. 4.5e-164;
Matches 516; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MMSRDTKTESQOQSGTSSSSSSAPQSYSSQSSSGTSSSLDTPVQDLASIPEDPEIDED 60
Db 1 MMSRDTKTESQOQSGTSSSSSSAPQSYSSQSSSGTSSSLDTPVQDLASIPEDPEIDED 60
Qy 61 IPQWGRWALGKGFNLHDCLEHEEVFGKDKCDYTFDIPVLNQTDYKTSKRHFRIQ 120
Db 61 IPQWGRWALGKGFNLHDCLEHEEVFGKDKCDYTFDIPVLNQTDYKTSKRHFRIQ 120
Qy 121 ELGHGHSRVANIEDLSNGTGFVNKEIIGKGRTPLTNNAEIALSLPTNKVFVFSLSVDD 180
Db 121 ELGHGHSRVANIEDLSNGTGFVNKEIIGKGRTPLTNNAEIALSLPTNKVFVFSLSVDD 180
Qy 181 QTIYPKDFIDKYIMSRPIGSGACGEVKLAFQSVCKVAVKIIISKRKFMTSSNEHPIS 240
Db 181 QTIYPKDFIDKYIMSRPIGSGACGEVKLAFQSVCKVAVKIIISKRKFMTSSNEHPIS 240
Qy 241 VDTETIILKLDHPICIIKIENPFDEDFYIIVLELMEGGEPLFDRVNVNSTRLEPIAKLYF 300
Db 241 VDTETIILKLDHPICIIKIENPFDEDFYIIVLELMEGGEPLFDRVNVNSTRLEPIAKLYF 300
Qy 301 YQMLLAQVYLHENGVIHRDLKPEVLLSTSECCIKITDFGQSKILGETSLMRTLCTGP 360
Db 301 YQMLLAQVYLHENGVIHRDLKPEVLLSTSECCIKITDFGQSKILGETSLMRTLCTGP 360
Qy 361 TYLAPEVLNTAGTTGYSSAVDCWSLGVILFVCLCGYPPFSEQNSIPLKNQIAEGKYTYI 420
Db 361 TYLAPEVLNTAGTTGYSSAVDCWSLGVILFVCLCGYPPFSEQNSIPLKNQIAEGKYTYI 420
Qy 421 AAARNVSEQAPDLVKNLLVVDPEQRLTTKQALEHPWLQDDSMKHTVERLMYGVVDHTWPP 480
Db 421 AAARNVSEQAPDLVKNLLVVDPEQRLTTKQALEHPWLQDDSMKHTVERLMYGVVDHTWPP 480
Qy 481 PIKKNIIIRKRGHEWDQDASTSSCSSEILPTSAEKRAKR 517
Db 481 PIKKNIIIRKRGHEWDQDASTSSCSSEILPTSAEKRAKR 517
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RESULT 3

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CHK2 HUMAN
ID CHK2 HUMAN STANDARD; PRT; 543 AA.
AC Q96017; Q9UGF0; Q9UGF1;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Serine/threonine-protein kinase Chk2 (EC 2.7.1.37) (Cds1).
GN Name=CHK2; Synonyms=CHK2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99108191; PubMed=9889122; DOI=10.1016/S0960-9822(99)80041-4;
RA Blasina A., van de Weyer I., Laus M.C., Luyten W.H.M.L., Parker A.E.,
RA McGowan C.H.;
RT "A human homologue of the checkpoint kinase Cds1 directly inhibits
RT Cdc25 phosphatase.";
RL Curr. Biol. 9:1-10(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99055399; PubMed=9836640; DOI=10.1126/science.282.5395.1893;
RA Matsuo S., Huang M., Elledge S.J.;
RT "Linkage of ATM to cell cycle regulation by the Chk2 protein kinase.";
RL Science 282:1893-1897(1998).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=99199255; PubMed=10097108; DOI=10.1073/pnas.96.7.3745;
RA Brown A.L., Lee C.-H., Schwarz J.K., Mitiku N., Plwnica-Worms H.,
```

Chung J.H.;

"A human Cdc61-related kinase that functions downstream of ATM protein
RT in the cellular response to DNA damage.";

Proc. Natl. Acad. Sci. U.S.A. 96:3745-3750(1999).

[4]

SEQUENCE FROM N.A.

TISSUE=Colon carcinoma;

Shao R.-G., Zhang H., Yu Q., Pommier Y.;

"Chk2/HucD31 cell cycle checkpoint protein kinase from human colon
RT carcinoma HT29 cells: regulation by autophosphorylation and DNA-
RT dependent protein kinase and inhibition by cell cycle regulatory
RT drugs.";

Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

[5]

SEQUENCE FROM N.A.

MEDLINE=200571165; PubMed=10591208; DOI=10.1038/990031;

Dunham I., Hunt A.R., Collins J.E., Bruskiewicz K., Beare D.M.,
RA Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,
RA Bagguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,
RA Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
RA Dhani P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
RA Evans K.D., Fey J.M., Fleming K., French L., Garner A.A.,
RA Gilbert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C.,
RA Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,
RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
RA Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,
RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,
RA McClell J., McLaren S., McMuray A.A., Milne S.A., Mortimore B.J.,
RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
RA Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,
RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,
RA Soderlund C., Spragon L., Steward C.A., Suleston J.E., Swann R.M.,
RA Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,
RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Matsuyama S.,
RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
RA Dorman A., Fang F., Fu Y., Hua A., Kenton S., Lai H., Lao H.I.,
RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,
RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,
RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
RA Zhan M., Zhang G., Chissoe S., Murray J., Miller N., Minx P.,
RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
RA Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing T.,
RA Scheet P., Walker C., Wansley A., Wohlmann P., Pepin K., Nelson J.,
RA Korf I., Bedell J.A., Hillier L.W., Mardis E., Waterston R.,
RA Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Saitta S.,
RA Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,
RA Edelman L., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P.,
RA Peyrard M., Kedra D., Serousi E., Franconi I., Bruder C.E.,
RA O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X.,
RA Khan A.S., Lane L., Tilahun Y., Wright H.;

"The DNA sequence of human chromosome 22.";

Nature 402:489-495(1999).

[6]

SEQUENCE FROM N.A.

TISSUE=Muscle;

MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;

R Straussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carncini P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullighy S.J.,
RA Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Sutterch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RL [7]
RN VARIANT THR-157, AND VARIANT COLON CANCER TRP-145.
RN MEDLINE=20085462; PubMed=10617473; DOI=10.1126/science.286.5449.2528;
RX Bell D.W., Varley J.M., Szlydo T.E., Kang D.H., Wahner D.C.R.,
RA Shannon K.E., Lubratovich M., Versalis S.J., Isselbacher K.J.,
RA Fraumeni J.F., Birch J.M., Li F.P., Garber J.E., Haber D.A.;
RT "Heterozygous germ line hCHK2 mutations in Li-Fraumeni syndrome.";
RL Science 286:2528-2531 (1999).
RN [8]
RN VARIANT THR-157.
RX PubMed=11461078; DOI=10.1054/bjoc.2001.1859;
RA Allinen M., Huusko P., Mantyniemi S., Launonen V., Winqvist R.;
RT "Mutation analysis of the CHK2 gene in families with hereditary breast
RL cancer.";
RL Br. J. Cancer 85:209-212 (2001).
RN [9]
RN VARIANTS OSTEOSARCOMA SER-17 AND LEU-85.
RX PubMed=11746983; DOI=10.1002/gcc.1207;
RA Miller C.W., Ikezoe T., Krug U., Hofmann W.K., Tavor S., Vegeena V.,
RA Takasaki K., Takeuchi S., Koefler H.P.;
RT "Mutations of the CHK2 gene are found in some osteosarcomas, but are
RT rare in breast, lung, and ovarian tumors.";
RL Genes Chromosomes Cancer 33:17-21 (2002).
RN [10]
RN VARIANTS PROSTATE CANCER LYS-64; PRO-145; ARG-167; CVS-180; HIS-180;
RX LYS-181; HIS-181; LYS-239; PHE-251; HIS-318; PRO-323; CVS-327 AND
RX LYS-476, AND VARIANT THR-157.
RX PubMed=12533788;
RA Dong X., Wang L., Taniguchi K., Wang X., Cunningham J.M.,
RA McDonnell S.K., Qian C., Marks A.F., Slager S.L., Peterson B.J.,
RA Smith D.I., Chevillie J.C., Blute M.L., Jacobsen S.J., Schaid D.J.,
RA Rindall D.J., Thibodeau S.N., Liu W.;
RT "Mutations in CHK2 associated with prostate cancer risk.";
RL Am. J. Hum. Genet. 72:270-280 (2003).
CC -1- FUNCTION: Controls cell cycle checkpoint. May participate in
CC transduction of the DNA damage and replication stress signals.
CC Inhibits CDC25C phosphatase by phosphorylating it on Ser-216,
CC preventing the entry into mitosis. May have a role in meiosis as
CC well.
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- ENZYME REGULATION: Kinase activity is up-regulated by
CC autophosphorylation. Rapidly phosphorylated in response to DNA
CC damage and to replication block.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- TISSUE SPECIFICITY: High expression is found in testis, spleen,
CC colon and peripheral blood leukocytes. Low expression is found in
CC other tissues.
CC -1- DISEASE: Defects in CHK2 are associated with Li-Fraumeni syndrome
CC (LFS) [MIM:151623]; a highly penetrant familial cancer phenotype
CC usually associated with inherited mutations in p53/TP53.
CC -1- DISEASE: Defects in CHK2 are found in some patients with prostate
CC cancer (Cap) [MIM:176807].
CC -1- DISEASE: Defects in CHK2 are found in some patients with
CC osteosarcoma (OSRC) [MIM:259500].
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. CDS1
CC subfamily.
CC -1- SIMILARITY: Contains 1 FHA domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collabora
CC between the Swiss Institute of Bioinformatics and the EMBL outstat
CC the European Bioinformatics Institute. There are no restrictions on
CC use by non-profit institutions as long as its content is in no
CC modified and this statement is not removed. Usage by and for commerc
CC


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Db 387 LCSTPYLAPEVLISNGTAGSVRAVCWSLGVLFICLSGYPPFSEHKTVQVSLKQITSG 446
QY 416 KYTIAAAARNVSEQAFDLVKNLLVVDPEQRLTKQALEHPWLQDDSMKHTVERLMYGVND 475
Db 447 KYNLPEVWTDVSEKALDLVKLLVVDPKARLTTEERALSHPWLQDEHMKKKFQDLVQEK 506
QY 476 HTWPPPI--KXNLIIRKGHWDP--QDASTSS-----CSEIL 507
Db 507 NLVPLPLAPAQTSQGRKPLELEADAESSKRLAVCKRAVL 545

RESULT 5
CHK2_MOUSE STANDARD; PRT; 546 AA.
AC Q92265;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Serine/threonine-protein kinase Chk2 (EC 2.7.1.37).
GN Names=Chk2; Synonyms=CHK2, Rad53;
OS Mus musculus (Mouse).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthazia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99055399; PubMed=9836640; DOI=10.1126/science.282.5395.1893;
RA Matsuo S., Huang M., Elledge S.J.;
RT "Linkage of ATM to cell cycle regulation by the Chk2 protein kinase.";
RL Science 282:1893-1897(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NMRI; TISSUE=Mammary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Controls cell cycle checkpoint. May participate in
transduction of the DNA damage and replication stress signals.
CC Inhibits CDC25 phosphatase by phosphorylating it, preventing the
entry into mitosis. May have a role in meiosis as well.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- ENZYME REGULATION: Kinase activity is up-regulated by
autophosphorylation. Rapidly phosphorylated in response to DNA
damage and to replication block (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. CDS1
subfamily.
CC -!- SIMILARITY: Contains 1 FHA domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial

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or send an email to license@isb-sib.ch).
CC
CC EMBL; AF086905; AAC83694.1; --
CC EMBL; BC056617; AAH56617.1; --
CC HSSP; OS6017; LGXC.
CC MGD; MGI:1355321; Chk2.
CC InterPro; IPR000253; FHA.
CC InterPro; IPR011009; Kinase like.
CC InterPro; IPR000719; Prot kinase.
CC InterPro; IPR008271; Ser thr pkin_AS.
CC InterPro; IPR008984; SMAD_FHA.
CC Pfam; PF00498; FHA; 1.
CC Pfam; PF00069; Kinase; 1.
CC ProDom; PD000001; Prot kinase; 1.
CC PROSITE; PS00006; FHA DOMAIN; 1.
CC PROSITE; PS00107; PROTEIN KINASE ATP; FALSE_NEG.
CC PROSITE; PS00111; PROTEIN KINASE_DOM; 1.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
CC ATP-binding; Cell cycle; Nuclear protein; Phosphorylation;
KW Serine/threonine-protein kinase; Transferase.
FT DOMAIN 117 179 FHA.
FT DOMAIN 224 490 Protein kinase.
FT NP_BIND 230 238 ATP (By similarity).
FT BINDING 253 253 ATP (By similarity).
FT ACT_SITE 351 351 Proton acceptor (By similarity).
SQ SEQUENCE 546 AA; 61088 MW; A7949EFB5572CDA4 CRC64;

Query Match 60.4%; Score 1637; DB 1; Length 546;
Best Local Similarity 63.0%; Pred. No. 4.5e-96;
Matches 320; Conservative 71; Mismatches 107; Indels 10; Gaps 5;

QY 9 ESQSQGTSSTSSSSSAP-OSYSSQSSSGTSLSDTVPQDLASIPDDPDEIDPQWGR 67
Db 40 ELSQYGGSSSTGTVPSSQSSSHSSGTLSTVSTQELCSIPEDQPEEPGPAPAR 99
QY 68 LVALKGFNLHDLHEEYVFGDKCDYTFDIPVNLQTRYKTYKRRHFRFOELGHGHS 127
Db 100 LVALQDGFNSLDCVNYWFGDKSCYCFDGLLRRTDKYRTYSKKHFRIFREMGPKNC 159
QY 128 RVANTEDLSGNTGFVNKEITIGKRTLPLTNNAEIALSLPTNKVFVFSDLSDVDOTIYPKD 187
Db 160 YIVYIEDHSGNGTFVNTIELIGKRCPLSNSEIALSLCRNKVFVFFDLTVDDQSVYPKE 219
QY 188 FIDKYMSPIGSGACGEVKLAFQKSVCKKAVKIISKRRKFKMTSSN-EHPISSVDETE 246
Db 220 LRDEYIMSKTSGACGEVKMAFERKTCQVAKIISKRRFALGSSREADTAPSVETE 279
QY 247 ILKLDHPICIIKENFFDSDFYIVLELMGEGELFDRVNVNSTRLEPIAKLYFYQMLA 306
Db 280 ILKLNHPICIIKIDVFAED-YIVLELMGEGELFDRVVGKRLKEATCKLYFYQMLA 338
QY 307 VOYLHENGVIHDLKPNVLLSSTSECCIKITDGCOSKILGETSLMRTLCTGPTVLAPE 366
Db 339 VOYLHENGVIHDLKPNVLLSSTSECCIKITDGCOSKILGETSLMRTLCTGPTVLAPE 398
QY 367 VLNTAGTCTSYSAVDCWSLGVLFVCLCGYPPFSEQNSNIPLNQKIAEGKYTIAAARN 426
Db 399 VLVSNGTAGSVRAVCWSLGVLFICLSGYPPFSEHKTVQVSLKQITSGKYNFPEVWD 458
QY 427 VSEQAFDLVKNLLVVDPEQRLTKQALEHPWLQDDSMKHTVERLMYGVND--TMPPEIKK 484
Db 459 VSEALDLVKLLVVDPKARLTTEERALSHPWLQDEYMKKKFQDLVQEKNSVTLVPAPAQ 518
QY 485 NIIRKGHWDP--QDASTSS-----CSEIL 507
Db 519 TSSQKRPLEVEGMPSTKRLSVCGAVL 546

RESULT 6
Q6QAll PRELIMINARY; PRT; 586 AA.
ID Q6QAll
AC Q6QAll;

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Db 61 SSETVSTGELSLIPEDQPEOEPEPTAPWALWALQDGFANLECVNDWYFGRDKS 120
Qy 93 CDYTEDIPVNLQDRTYKTKRHRIFQELGHGHRVANIEDLSNGTGFVNKEIIGKGR 152
Db 121 CEYCFDEPLKRTDKYRTYKTKRHRIFREVGPKNSYIAIEDHSGNGTFVNTLVGKGR 180
Qy 153 LPLTNNAETALSIPVNLQDRTYKTKRHRIFQELGHGHRVANIEDLSNGTGFVNKEIIGKGR 212
Db 181 RPLNNNSEIATLSLRNKVFFDLTVDDQSVYPKALRDEYIMSKTILSGACGEVKLAFER 240
Qy 213 SVCKKAVAKIISKRFKPMNTSSNEHP- ISVDTEIEILKLDHPICIIKENFFDSDFYVI 271
Db 241 KTKCKVAIKIISKRFKPMNTSSNEHP- ISVDTEIEILKLDHPICIIKENFFDSDFYVI 299
Qy 272 VLEMEGGELFDRVNVNSTRLEPIAKLYFYQMLLAVQYLHENGVIHRDLKPNVLLSSTS 331
Db 300 VLEMEGGELFDRVNVNSTRLEPIAKLYFYQMLLAVQYLHENGVIHRDLKPNVLLSSTS 336
Qy 332 EBCCKITIDFGOSKILGETSLMRTLCGTPTTYPYLAPEVNTAGTYGSSAVDCWSLGVILPV 391
Db 337 -----ITDFGHSKILGETSLMRTLCGTPTTYPYLAPEVNTAGTYGSSAVDCWSLGVILPV 390
Qy 392 CLCGVPPFSEQNSNIPLNQIAEGKYTYIAAARNVSECAFVKNLAVVDPQRLTTKQ 451
Db 391 CLSGVPPFSEHRTQVSLKQDITSGKNFIPVMAEVSEKALDLVKKLLVVDPRKPTTEE 450
Qy 452 ALEHWPLOQDSMKHTVERIMYGVDMTPPP-----IKNNIIRKGEHWDDQDASTSS-----C 503
Db 451 ALRHPWLOQDSMKHTVERIMYGVDMTPPP-----IKNNIIRKGEHWDDQDASTSS-----C 503
Qy 504 SEIL 507
Db 511 AAVL 514

RESULT 8
Q902Y5 PRELIMINARY; PRT; 503 AA.
AC Q902Y5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Protein kinase Chk2.
GN ORFNames=zgc:55865;
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Chou C.-M., Liu J.-H., Huang C.-J.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AF265346; AAK52419.1; -.
DR HSSP; P49137; INXK.
DR ZFIN; ZDB-GENE-030131-8942; zgc:55865.
DR GO; GO:0005524; F-ATP binding; IEA.
DR GO; GO:0004674; F-protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0008468; P:protein amino acid phosphorylation; IEA.
DR Pfam; PF00498; FHA; 1.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00240; FHA; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS50006; FHC DOMAIN; 1.
DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 503 AA; 56699 MW; BC01BF3D84CEC71 CRC64;

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Query Match 48.6%; Score 1317.5; DB 2; Length 503;
Best Local Similarity 53.7%; Pred. No. 9.1e-76;
Matches 264; Conservative 86; Mismatches 125; Indels 17; Gaps 7;

Qy 3 SRDTKTESQ-OSQSTSSSSSSSAPOSYSQ--SSSGTSLSSLDTPVQDLASIPEDPEIDE 59
Db 8 SGESOSQTSQTSOPASSSSSAPTSSSQSGSSGSLSSVDTPVQELQSIPEDEE--E 65
Qy 60 DIPQWGLMALGKGLNHDCLHBEYVFRGRKCKDYTFDIPVLNQTDRTYKTKRHRIF 119
Db 66 VQPVQWGRRIIPLKQFQSVLNCNTENQYSGRDKRCDSFSNLSILKSPYNTYKSKHRIF 125
Qy 120 QELGHGHRVANIEDLSNGTGFVNKEIIGKGRPLTNNAETALSIPVNLQDRTYKTKRHRIF 179
Db 126 RD-----ENLYLELDLSNGTGVDDDEKLGNKQSLSSNVTALEAQKHQVFMFIDKQAD 180
Qy 180 DOTIYPKDFIDKYIMSRPIGSGACGEVKLAFKSVCKKAVAKIISKRF-KNNTSSNEHP 238
Db 181 DQANLPLEFSKYHARKIGTGVCGEVLAKIEKETFKKVALKTKINKHDFPSIGTATR--- 237
Qy 239 ISVDTEIEILKLDHPICIIKENFFDSDFYIVLELMEGGELFDRVNVNSTRLEPIAKL 298
Db 238 -NABREIEILKLDHPICIIKTEDFYQTESYVIVLEYIEGGELFGRIKAKKLEEDIACL 296
Qy 299 VFYQMLLAVQYLHENGVIHRDLKPNVLLSSTSECCIKITDFGOSKILGETSLMRTLCG 358
Db 297 VFYQMLKAVEYLHNGGIHRDLKPNVLLSHDDICLIKITDFNQSILKEESSLMKTLGC 356
Qy 359 TPTYLAPVNLNTAGTYGSSAVDCWSLGVILFVCLGYPFPPSEONSNIPLKNQIAEGKYT 418
Db 357 TPTYVPEVFTASTVGTAKVDYWSLGVILFICLGGYPPFNTCTTWSVRQIINGEYR 416
Qy 419 YIAAARNVSEQAFDLVKNLAVVDPQRLTTKQALEHWPLOQDSMKHTVERIMYGVDMTPM 478
Db 417 FIPSQMKVNSNEAKDLVKLLVDPQKRLSVEEALEHWPLOQDRVQANQLMN--PGAA 474
Qy 479 PPPIKKNIRKR 490
Db 475 NQMPREATRKR 486

RESULT 9
Q803E2 PRELIMINARY; PRT; 503 AA.
AC Q803E2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CHK2 checkpoint homolog.
GN ORFNames=zgc:55865;
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=AB; TISSUE=whole body;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton G., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

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QY 332 EECIKITDFGSKILGETSLMRTLCGTPYLAPEVLNTAGTTGYSSAVDCWSLGVILFV 391
Db 269 EDCIKITDFGSKILGETSLMRTLCGTPYLAPEVLNTAGTGYSSAVDCWSLGVILFI 328
QY 392 CLCGYPPFSEQNSNIPKQIAEGKTYIAAAARNVSEQAFDLVKNLLVVDPQRITTKQ 451
Db 329 CLSGYPPFSEHRTQVSLKQITSGKYNFPEVWAEVSEKALDLVKKLLVDPKARFTTEE 388
QY 452 ALEHPWLQDSMKHTVERLMYGVHDHTMPPP---IKNNIRKHEWDQDASTSS-----C 503
Db 389 ALRHPWLQDDMKRKTQDLLEENESTALPQVLAQPSTSRKRPREGAEAGETTKRPVAVC 448
QY 504 SEIL 507
Db 449 AAVL 452

RESULT 11
Q9HBS5
ID Q9HBS5 PRELIMINARY; PRT; 322 AA.
AC Q9HBS5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,
RA Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,
RA Yu J., Han L.H.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; A217975; A217975.1; -.
DR HSSP; P49137; INXK.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC_1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS0108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Hypothetical protein; Kinase;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 322 AA; 36157 MW; D31257F4B9652438 CRC64;

Query Match 39.3%; Score 1066; DB 2; Length 322;
Best Local Similarity 63.8%; Pred. No. 5.4e-60;
Matches 206; Conservative 44; Mismatches 63; Indels 10; Gaps 4;

QY 194 MSRPISGAGGEVKLAFQSVCKKAVKIISKKEKMTSSNEHP-LSVDTEIILKLD 252
Db 1 MSKTLGSGAGGEVKLAFQSVCKKAVKIISKKEKMTSSNEHP-LSVDTEIILKLD 60
QY 253 HPCIIKIENPFDSDFYIIVLELMEGGELFDRVNVNSTRLEPIAKLYFYQMLLAVOYLHE 312
Db 61 HPCIIKIENPFDAED-YIIVLELMEGGELFDRVNVNSTRLEPIAKLYFYQMLLAVOYLHE 119
QY 313 NGVIHRDLKPENVLLSGTSEBCCIKITDFGQSKILGETSLMRTLCGTPYLAPEVLNTAG 372
Db 120 NGIIHRDLKPENVLLSQBEDCLIKITDFGSKILGETSLMRTLCGTPYLAPEVLVSVG 179
QY 373 TTGYSSAVDCWSLGVILFVCLCGYPPFSEQNSNIPKQIAEGKTYIAAAARNVSEQAF 432
Db 180 TAGYNRAVDCWSLGVILFVCLSGYPPFSEHRTQVSLKQITSGKYNFPEVWAEVSEKAL 239
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QY 433 DLVKNLLVDPQRITTKQALEHPWLQDSMKHTVERLMYGVHDHTMPPP---IKNNIRK 489
Db 240 DLVKNLLVDPQRITTKQALEHPWLQDSMKHTVERLMYGVHDHTMPPP---IKNNIRK 299
QY 490 RGEHWDQDASTSS-----CSEIL 507
Db 300 RPREGEAGETTKRPVAVCAVL 322

RESULT 12
Q6QA08
ID Q6QA08 PRELIMINARY; PRT; 339 AA.
AC Q6QA08;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Protein kinase Chk2 transcript variant del9-12.
GN Name=CHK2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Breast carcinoma;
RA Staalesen V., Falck J., Geisler S., Bartkova J., Borresen-Dale A.-L.,
RA Lukas J., Lillehaug J.R., Lonning P.E.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY551300; AAS58461.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000253; FHA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008984; SMAD_FHA.
DR Pfam; PF00498; FHA; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00240; FHA; 1.
DR SMART; SM00220; S_TKC_1.
DR PROSITE; PS50006; FHA_DOMAIN; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW Kinase.
SQ SEQUENCE 339 AA; 38125 MW; CAE0E59DF0308393 CRC64;

Query Match 37.3%; Score 1012.5; DB 2; Length 339;
Best Local Similarity 60.2%; Pred. No. 1.5e-56;
Matches 203; Conservative 47; Mismatches 56; Indels 31; Gaps 5;

QY 2 MSRDITKTESQ-----QSQGTSSSSSSSAP-QSYQSSSSSGL 37
Db 1 MSRESDVRAQSHGSSACSQPHGVTQSGSSSQGSSSTSTWPNSSSHSSSGL 60
QY 38 SSLDTPVPQDLASI-----PEPDEIDIPQWGRWLWALGKGLNHDCLHEEVVFCRDKK 92
Db 61 SLEIVTSVQELYSIPEDQEPEDQEPPEPTPAWRLWALQDGFANLECVNDYWFGRDKS 120
QY 93 CDYTFDIPVLNQTDRKYTSKHFRIFOELGHGHSRVANIEDLSNGTTFVNKEIIGKRT 152
Db 121 CEYCFDEPLLRKTKYRYSKKHFRIFREVGPKNSYIAVEDHSGNGTFTVNLVKGKR 180
QY 153 LPLTNNAETALSIPNKVVFSDLSVDDOTIYPKDFIDKYIMSRPIGSGACGEVKLAFQ 212
Db 181 RPLNNSETALSLSRNKVFVFDLTVDQSVVPKALRDEYIMSKTSGSACGEVKLAF 240
QY 213 SVCKKAVAKIISKRFKMTSSNEHP-LSVDTEIILKLDHPCIIKIENPFDSDFYI 271
Db 241 KTCKKVAKIISKRFATGSAAREADPALNVETEILKLNHPCIIKIENPFDAED-YI 299
QY 272 VLELMEGGELFDRVNVNSTRLEPIAKLYFYQMLLAVQ 308
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RESULT 13

ID	LOC_DROME	STANDARD;	PRT;	476 AA.
AC	O61267; O61268; P91876; Q89ZS3;			
AD	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	25-JAN-2005 (Rel. 46, Last annotation update)			
DE	Ovarian-specific serine/threonine-protein kinase Lok (EC 2.7.1.37)			
GN	(Loki protein) (dMNK).			
GN	Name=lok; ORFNames=CG10895;			
OS	Drosophila melanogaster (Fruit fly).			
OS	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;			
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
OC	Ephyroidea; Drosophilidae; Drosophila.			
OX	NCBI_TaxId=7227;			
RP	[1]			
RP	SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT), FUNCTION, SUBCELLULAR			
RP	LOCATION, TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.			
RC	STRAIN=Canton-S; TISSUE=Embryo;			
RC	MEDLINE=98175876; PubMed=9507063; DOI=10.1016/S09925-4773(97)00200-1;			
RX	Olshi I., Sugiyama S., Ocani H., Yamamura H., Nishida Y., Minami Y.;			
RT	"A novel Drosophila nuclear protein serine/threonine kinase expressed			
RT	in the germline during its establishment.";			
RL	Mech. Dev. 71:49-63(1998).			
RP	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM SHORT).			
RC	STRAIN=oregon-R; TISSUE=ovary;			
RC	Laroche S., Suter B.;			
RT	"Identification of a novel ovarian specific protein kinase.";			
RL	Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.			
RP	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Berkley;			
RX	MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;			
RA	Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,			
RA	Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,			
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,			
RA	Sutton G.G., Wortman J.R., Vandell M.D., Zhang Q., Chen L.X.,			
RA	Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,			
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,			
RA	Abell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,			
RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,			
RA	Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,			
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,			
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,			
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,			
RA	de Fabos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,			
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,			
RA	Dubin K.J., Evangelista C.C., Ferraz C., Ferreria S., Fleischmann W.,			
RA	Fosler K., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,			
RA	Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,			
RA	Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,			
RA	Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwa C.,			
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,			
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Rulp D., Lai Z.,			
RA	Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,			
RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,			
RA	Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,			
RA	Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,			
RA	Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,			
RA	Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,			
RA	Reiner K.C., Remington K., Saunders R.D.C., Scheeler F., Shen H.,			
RA	Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,			
RA	Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,			
RA	Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,			
RA	Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,			
RA	Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,			
RA	Ye J., Yeh R.-F., Zaveri J.-S., Zhan M., Zhang G., Zhao Q., Zheng L.,			
RA	Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,			

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OM protein - protein search, using sw model

Run on: July 7, 2005, 12:33:18 ; Search time 162 Seconds
(without alignments)
1234.291 Million cell updates/sec

Title: US-10-618-173-2

Perfect score: 2712

Sequence: 1 MMSRDTKTESQSQSGTSSSS.....ASTSSCSBILPTSAEKRAKR 517

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2712	100.0	517	5	AAB47789 Protein k
2	1656	61.1	542	4	AAG68375 Human Chk
3	1655.5	61.0	543	2	AAY06204 Human che
4	1655.5	61.0	543	2	AAY05765 Novel hum
5	1655.5	61.0	543	5	AAM48995 Human Chk
6	1655.5	61.0	543	5	ABG30701 Human che
7	1655.5	61.0	543	8	ADL32561 Human Chk
8	1655.5	61.0	543	8	ADM72213 Human TFS
9	1655.5	61.0	543	8	ADO44010 Amino aci
10	1655.5	61.0	543	8	ADQ09232 Human CHE
11	1651.5	60.9	543	5	AAM48996 Human Chk
12	1643.5	60.6	543	3	AAY67968 Human cel
13	1624	59.9	586	8	ADM61455 Human KPP
14	1499	55.3	514	8	AAM48994 Human Chk
15	1499	55.3	514	8	ADL32563 Human Chk
16	838.5	30.9	459	4	ABG5298 Drosophil
17	621	22.9	513	8	ADN18925 Bacterial
18	603	22.2	356	4	AAB84360 Amino aci
19	600.5	22.1	355	4	AAB50055 Murine de
20	600.5	22.1	355	4	AAE11777 Human Chk
21	600.5	22.1	355	4	AAM41268 Human pol
22	600.5	22.1	355	5	ABG08178 Human Cam
23	600.5	22.1	357	4	AAE11768 Human kin
24	600.5	22.1	357	8	ADJ75440 Marker ge
25	600.5	22.1	357	8	ADQ15044 Human can

RESULT 1

AAB47789

ID AAB47789 standard; protein; 517 AA.

XX AAB47789;

AC AAB47789;

XX 04-MAR-2002 (first entry)

XX Protein kinase Cds1.

XX Protein kinase: Xenopus; Cds1; Xcds1; DNA damage checkpoint; cell cycle;

XX Cdc25; forkhead-associated domain; FHA domain; ATM; ATR; DNK-PK; Chk2;

XX human; mitotic delay.

XX Xenopus laevis.

XX WO200183703-A2.

XX 08-NOV-2001.

XX 04-MAY-2001; 2001WO-US014646.

XX 04-MAY-2000; 2000US-0202028P.

XX (CALY) CALIFORNIA INST OF TECHNOLOGY.

XX Dumphy WG, Guo Z;

XX WPI: 2002-066528/09.

XX N-PSDB; AAI72072.

XX Novel polypeptide for regulating cell cycle progression, which is

XX activated and phosphorylated in response to double-stranded DNA useful

XX for diagnosing and treating cell proliferative disorder.

XX Claim 2; Fig 2; 75pp; English.

XX This sequence shows the protein kinase, Xenopus Cds1 (Xcds1) which plays
XX a role in DNA damage checkpoint and regulating progression of cell cycle.
XX The protein is characterized as phosphorylating Cdc25 or its homolog,
XX having a molecular mass of 58 kD, 517 amino acids, SQ/TQ motifs at the
XX amino terminal region, a carboxyl terminal kinase domain and an amino
XX terminal forkhead-associated (FHA) domain. Xcds1 phosphorylates Cdc25 on
XX Ser287 in the 14-3-3 binding site, which inhibits its activity. Xcds1 is
XX activated by poly(dT)40. When Xcds1 is phosphorylated in extracts
XX containing poly(dT)40, hyperphosphorylated Cds1 shows a five- to six-fold
XX increase over background in its kinase activity towards GST-Cdc25[254-
XX 316]-WT. The SQ/TQ motifs at the amino terminal end of Xcds1 are

CC potential substrates for kinases such as ATM, ATR and DNK-PK that are
CC involved in checkpoint pathways. The C-terminal kinase domain is the most
CC conserved region of Xcd1 when compared to Chk2, the human homologue of
CC Xcd1. Cdel protein or mRNA is useful for diagnosing a Cdel-associated
CC disorder in a subject, by determining the level of Cdel mRNA or protein
CC expression in the subject, where a low level of Cdel in the subject
CC compared to a control is indicative of a Cdel-associated disorder.
CC Oligonucleotides (see AA172073-75) which form double stranded regions
CC with Xcds DNA are useful for increasing mitotic delay in a vertebrate
CC cell

XX Sequence 517 AA;

Query Match 100.0%; Score 2712; DB 5; Length 517;
Best Local Similarity 100.0%; Pred. No. 8e-248;
Matches 517; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMSRDTKTESQSQSGTSSSSSSAPQSYSSQSSSGTSSLDTPVPQDLASIPEDPEIDED 60
DB |||||
QY 1 MMSRDTKTESQSQSGTSSSSSSAPQSYSSQSSSGTSSLDTPVPQDLASIPEDPEIDED 60
DB |||||
QY 61 IPQPGRLWALGKFLNHDCLHEEVYVFGDKKCDYTFDIPVLNQTDRYKTKRHRIFQ 120
DB |||||
QY 61 IPQPGRLWALGKFLNHDCLHEEVYVFGDKKCDYTFDIPVLNQTDRYKTKRHRIFQ 120
DB |||||
QY 121 ELCHGHSRVANTEDLSGNGTFFVKEIIGKGRTPLTNNAEIALSLPTNKVFVFSLSVDD 180
DB |||||
QY 121 ELCHGHSRVANTEDLSGNGTFFVKEIIGKGRTPLTNNAEIALSLPTNKVFVFSLSVDD 180
DB |||||
QY 181 QTIYPKDFIDKYMIRPIGSGAGCVKLAFAQSVCKVAVKIIISKRKFQMTSSNEHPIS 240
DB |||||
QY 181 QTIYPKDFIDKYMIRPIGSGAGCVKLAFAQSVCKVAVKIIISKRKFQMTSSNEHPIS 240
DB |||||
QY 241 VDETEILKLDHPCLIIKIENFDSEDFYIIVLELMGEGELFDRVNSTRLREPTAKLYF 300
DB |||||
QY 241 VDETEILKLDHPCLIIKIENFDSEDFYIIVLELMGEGELFDRVNSTRLREPTAKLYF 300
DB |||||
QY 301 YQMLLAVQYLHENGVIHRLDKPENVLSSSTSECCIKITDFGOSKILGETSLMRTLCTGP 360
DB |||||
QY 301 YQMLLAVQYLHENGVIHRLDKPENVLSSSTSECCIKITDFGOSKILGETSLMRTLCTGP 360
DB |||||
QY 361 TYLAPEVLNTAGTTGYSSAVDCMSGLVILFVCLCGYPPFSEQNSNIPLNQIAEGKYTI 420
DB |||||
QY 361 TYLAPEVLNTAGTTGYSSAVDCMSGLVILFVCLCGYPPFSEQNSNIPLNQIAEGKYTI 420
DB |||||
QY 421 AAARNVSEQAFDLVKNLLVDPPEQLTTKQALEHPWLQDDSMKHTVERLMYGVDDHTMPP 480
DB |||||
QY 421 AAARNVSEQAFDLVKNLLVDPPEQLTTKQALEHPWLQDDSMKHTVERLMYGVDDHTMPP 480
DB |||||
QY 481 PIKKNIRKRGHEWDQDASTSSCSEILPTSAKRAKR 517
DB |||||
QY 481 PIKKNIRKRGHEWDQDASTSSCSEILPTSAKRAKR 517
DB |||||

RESULT 2

AA68375
ID AAG68375 standard; protein; 542 AA.

XX AAG68375;

XX 13-JUL-2001 (first entry)

DE Human Chk2 kinase protein sequence.

XX Human; Cdc25C; Chk1; Chk2; G2 checkpoint; cell cycle regulation; cancer;
KW cell proliferation; apoptosis.

OS Homo sapiens.

PN WO200121771-A2.

XX 29-MAR-2001.

XX

PF 21-SEP-2000; 2000WO-IB001438.
XX
PR 22-SEP-1999; 99JP-00269398.
PR 30-NOV-1999; 99JP-00340322.
XX
PA (CANB-) CANBAS CO LTD.
XX
PI Suganuma M, Kawabe T;
XX
XX WPI; 2001-343125/36.
DR
XX
XX Isolated or recombinant polypeptide of 7-11 amino acids, useful for
PT treating cell proliferative disorders, e.g. to stop the growth of, or
PT kill cancer cells, by disrupting the G2 cell cycle arrest checkpoint.
PT
XX Disclosure; Page 26; 126pp; English.
XX
CC The present invention describes a number of peptides which disrupt the G2
CC cell cycle checkpoint when administered to a cell. They act by inhibiting
CC Chk2 (the sequence of which is shown here) and Chk1 kinases, and may be
CC derived from Cdc25C. The peptides are useful in the treatment of cell
CC proliferation diseases, such as cancer, as the inhibition of the Chks
CC allows DNA damage and induces apoptosis
XX
XX Sequence 542 AA;

Query Match 61.1%; Score 1656; DB 4; Length 542;
Best Local Similarity 60.0%; Pred. No. 1.4e-147;
Matches 326; Conservative 74; Mismatches 105; Indels 38; Gaps 7;

QY 2 MSRDTKTESQSQSGTSSSSSSAPQSYSSQSSSGTSSLDTPVPQDLASIPEDPEIDED 38
DB |||||
QY 1 MSRESDEVAQSHGSSACSPHGSVTSQSGSSSQSGISSTSTMPNSQSSSHSSGTL 60
DB |||||
QY 39 SLDTVPVQDLASIPEDPEIDEDIPQWGRUWALGKFLNHDCLHEEVYVFGDRKK 93
DB |||||
QY 61 SLETVSTQELYSIPEDQEPDEPEPTAPARLWALQDGFANLECVNDNWFGRDKSC 120
DB |||||
QY 94 DYTEDIPLVNTQDRYKTKRHRIFOEELGHGHSRVANIEDLSGNGTFFVKEIIGKGR 153
DB |||||
QY 121 EYCFDEPLKRTDKYRTYKSKHRIFRFGVGNPNYIAYIEDHSGNGTFFVTELGVGKRR 180
DB |||||
QY 154 PLTNNAEIALSLPTNKVFVFSLSVDDQTIYPKDFIDKYMIRSRPTGSGACGEVKLAFOKS 213
DB |||||
QY 181 PLNNSEIALSLRNKVFVFFDLTVDDQSVYFKALRDEYIMSKTSGACGEVKLAFERK 240
DB |||||
QY 214 VCKKAVKIIISKRKFQMTSSNEHP- ISVDTEILKLDHPCLIIKIENFDSEDFYIIV 272
DB |||||
QY 241 TCKVAIKIIISKRKFAIGSAREADPALNVETEIELKLNHPCTIIKKNFDEAD-YIIV 299
DB |||||
QY 273 LELMEGGELEFDRVNSTRLREPIAKLYFQMLLAVQYLHENGVIHRLDKPENVLSSSTSE 332
DB |||||
QY 300 LELMEGGELEFDRVGNKRLKEATCKLYFQMLLAVQYLHENGIIHRLDKPENVLSSQEE 359
DB |||||
QY 333 ECCIKITDFGOSKILGETSLMRTLCTGPTYLAPEVLNTAGTTGYSSAVDCMSGLVILFVC 392
DB |||||
QY 360 DCLIKITDFGHSKILGETSLMRTLCTGPTYLAPEVLVSVGTAGYNRAVDCMSGLVILFIC 419
DB |||||
QY 393 LCGYPPFSEQNSNIPLNQIAEGKYTIYAAARNVSEQAFDLVKNLLVDPPEQLTTKQOA 452
DB |||||
QY 420 LSGYPPFSEHRTQVSLKQDITSGKYNFIPVNAEYSEKALDLVKKLLVDPPEKARFTTEA 479
DB |||||
QY 453 LEHPWLQDDSMKHTVERLMYGVDDHTMPPP---IKKNIRKRGHEWDQDASTSS---CS 504
DB |||||
QY 480 LHPWLQDDMKRKFQDILLSEENESTALPQVLAQPSSTSRKPRPREGEAETTKRPAVCA 539
DB |||||
QY 505 EIL 507
DB :
DB 540 AVL 542

RESULT 3
AAY06204

ID AAY06204 standard; protein; 543 AA.
 AC AAY06204;
 DT 16-AUG-1999 (first entry)
 XX Human checkpoint kinase hCDS1.
 DE
 XX Checkpoint kinase; hCDS1; human; DNA damage; proliferative disease;
 KW cancer; therapy.
 XX Homo sapiens.
 XX WO9925843-A2.
 XX 27-MAY-1999.
 XX 21-OCT-1998; 98WO-EP006981.
 XX 22-OCT-1997; 97GB-00022320.
 XX (SCRI) SCRIPPS RES INST.
 XX (JANC) JANSSEN PHARM NV.
 XX Luyten WHML, Parker AE, McGowan C, Blasina A;
 XX WPI; 1999-338010/28.
 XX N-PSDB; AAX58793.
 XX New human kinase used for treatment of cancer and proliferative diseases.
 XX Claim 9; Fig 2; 39pp; English.
 XX The present sequence represents a novel human checkpoint kinase, termed
 CC hCDS1, that acts in coordination with Cdc25 in the DNA damage checkpoint.
 CC The sequence is predicted from a cDNA (see AAX58793) isolated from a SK-N
 CC -MC neuroblastoma cDNA library. The predicted protein is 28% identical to
 CC the cdc1 protein of S. pombe. A 2.2 kb transcript is expressed in testis
 CC and in 8 human cancer samples examined. hCDS1, its inhibitors and
 CC activators, are useful for treating cancer or proliferative disease
 CC (claimed). Inhibitors and activators of the kinase activity can also be
 CC used in anti-cancer therapy, particularly by increasing susceptibility of
 CC cancer cells to chemotherapy and/or radiotherapy (claimed). hCDS1 is
 CC useful for modifying DNA damage checkpoint activity of a cancer cell
 CC (claimed)
 XX
 XX Sequence 543 AA;
 SQ
 Query Match 61.0%; Score 1655.5; DB 2; Length 543;
 Best Local Similarity 59.9%; Pred. No. 1.6e-147;
 Matches 326; Conservative 74; Mismatches 105; Indels 39; Gaps 7;
 QY 2 MSRDVTXESQ-----QSQGTSSSSSSAP-QSYSSSSGTL 37
 DB 1 MRESDEVAQSHGACACPHGCVTQSGSSSQSGISSTSTMPNSQSHSSGTL 60
 QY 38 SLDITVPQDLASI-----PEDPEIDIPQPMGRMLWALGKFLNHDCLHEEYVFGDRKK 92
 DB 61 SLETVSTQELYSIPEDQEPDQEPPEPTAPARLWALQDGFANLECVNDNYWFGDRKS 120
 QY 93 CDYTFDIPVLNQTRKYTKHFRIFQELGHGSHRVANIEDLSNGTFTVNEIKGRT 152
 DB 121 CEYCFDEPLLKRTDKYTKYKHHFRIFREVGPKNSYIAVIEDHSGNGTFTVNEIKGRT 180
 QY 153 LPLTNAETALSPTNKVFPVPSDLSDDTIYKDFIKYMSRPTGSGACGEVLAFOK 212
 DB 181 RPLNNSEIALSLRKNVFFVFDLTVDQSVYKALRDEITMSKTUGSGACGEVLAFOK 240
 QY 213 SVCKVAVKIISKRFKAMNTSNEHP-ISVDTIELKLLDHPICIIKNFFDSEDFYII 271
 DB 241 KTCKVAVKIISKRFKFAIGSAREADPALNVETIELKLLNHPICIIKNFFDAED-YII 299
 QY 272 VLEMEGGELFDRVNVNSTRLEPIAKLYFYQMLLAVQYLHENGVIHRDLKPENVLSSTS 331

Db 300 VLEMEGGELFDRVNVNSTRLEPIAKLYFYQMLLAVQYLHENGVIHRDLKPENVLSSOE 359
 QY 332 EECCKITDYGOSKILGETSLMRTLCGTPTYLAPVNLTAGTGYSSAVDCWSLGVILFV 391
 Db 360 EDCLIKITDGHGKILGETSLMRTLCGTPTYLAPVNLTAGTGYSSAVDCWSLGVILFI 419
 QY 392 CLCGYPPPESEQNSNIPLNQIAEGKYTYIAAARNVSEQAFDLVKNLLVVDPEQRUTTKQ 451
 Db 420 CLSGYPPPESEHRTQVSLKQITSGKYNFTPEVMAEVSERKALDLVKKLLVVDPKARFTTE 479
 QY 452 ALEHPLQDDSMKHTVERLMYGVHDHTMPP-----IKGNIIRKRGHEWDQDASTSS-----C 503
 Db 480 ALRHPWLQDDMKRRKFDLLSEENSTALPQVLAQFSTSRKRPREGAEGAEETTKRPAVC 539
 QY 504 SEIL 507
 Db 540 AAVL 543
 RESULT 4
 AAY05765
 ID AAY05765 standard; protein; 543 AA.
 XX AAY05765;
 AC AAY05765;
 XX 02-AUG-1999 (first entry)
 XX Novel human checkpoint kinase hCDS1.
 DE
 XX Cell cycle checkpoint kinase; human; hCDS1; cell proliferation; cancer;
 KW therapy; chemotherapy; adjunct.
 XX Homo sapiens.
 XX WO9920747-A2.
 XX 29-APR-1999.
 XX 21-OCT-1998; 98WO-EP006982.
 XX 22-OCT-1997; 97GB-00022320.
 XX (JANC) JANSSEN PHARM NV.
 XX Luyten WHML, Parker AE;
 XX WPI; 1999-288300/24.
 XX N-PSDB; AAX25464.
 XX Novel human cell cycle checkpoint kinase hCDS1, useful for treating cell
 XX proliferation diseases, e.g. cancer.
 XX Claim 2; Page 33-34; 35pp; English.
 XX The present sequence represents hCDS1, a novel human cell cycle
 XX checkpoint kinase that acts in coordination with Cdc25 at the DNA damage
 XX checkpoint, rather than the replication checkpoint as found in yeast. The
 XX hCDS1 sequence was predicted from hCDS1 cDNA (see AAX25464) that was
 XX obtained from a human SK-N-MC neuroblastoma cDNA library. It shows 28%
 XX identity with cdc1 protein of S. pombe, 28% identity to RAD53 and 27%
 XX identity to the DUN1 kinase of S. cerevisiae. Northern blot analysis
 XX identified a single transcript of about 2.2 kb expressed in testis and in
 XX 8 human cancer samples examined. The characterization of hCDS1 and the
 XX elucidation of its role in the DNA damage checkpoint allows for the
 XX preparation of pharmaceuticals and therapeutic methods for acting as an
 XX adjunct to chemotherapy of cancer. Thus, pharmaceutical formulations
 XX incorporating hCDS1 cDNA, RNA, antisense molecules, hCDS1 protein,
 XX antibodies against the protein, or other therapeutics identified in
 XX assays of the invention, can be administered in conjunction with any
 XX suitable chemotherapy agent to act as an adjunct to the main action of
 XX the chemotherapy agent

XX		New gene encoding a protein for inhibiting human Chk2 phosphoenzyme activity.
PT		
XX		
PS	Disclosure; Page 20-23; 36pp; Japanese.	
CC	The present invention provides the protein and coding sequences of a human Chk2 phosphoenzyme inhibitor. The sequences can be used in the chemotherapy of cancers. The present sequence is a protein described in the exemplification of the invention	
XX		
SQ	Sequence 543 AA;	
	Query Match 61.0%; Score 1655.5; DB 5; Length 543; Best Local Similarity 59.9%; Pred. No. 1.6e-147; Matches 326; Conservative 74; Mismatches 105; Indels 39; Gaps 7;	
QY	2 MSRDTKTESQ-----SQGTSSSSSSAP-QSYSGSSSGTL 37 ::: - ::: -	
DB	1 MSRESDEAQQHGSHGSACSPHGSVTQSQSSSQSGISSTSTMPNSSQSHSSGTL 60 ::: - ::: -	
QY	38 SSLDTPVPQDLASI-----PEDPEIDEDIPOPWGRWLALGKGFNLHDCLEHEEVVFGDRDK 92 ::: - ::: -	
DB	61 SSLETVSTQELYSIPEDQEPDEPPTAPARLWALQGDFANLECVDNDNTWFGRDKS 120 ::: - ::: -	
QY	93 CDYTFDIPLVAQLDTKYTYSKRHFRIFOELGHGHSRVANIETLSGNCTFVNKEIIIGKRT 152 ::: - ::: -	
DB	121 CEYCFDEPLLKRTDKYRTYSKKHFRIPREVGPKNSYAIYIEDHSGNCTFVNTELVGKGKR 180 ::: - ::: -	
QY	153 LPLTNNAIALSLPTNKVFVSDDLSDVDDOTIYPKDFIDKYIMSRPIGSGACGEVKLAFOK 212 ::: - ::: -	
DB	181 RPLNNSEIALSLRNKVFPVFDLTVDQSVYPKALRDEVIMSKTGLSGACGEVKLAFAER 240 ::: - ::: -	
QY	213 SVCKKAVAKIISKRFKMTSSNEHP-ISVDTEIEILKLDHPICIIKIENFFDSEDIFYI 271 ::: - ::: -	
DB	241 KTCKKVAIKIISKRFPAIGSAREADPALNVETEIEILKLNHPICIIKINFFDAED-YII 299 ::: - ::: -	
QY	272 VLELMEGGELFDRVNVSTRREP IAKLYFYOMLLAVOYLHENGVIHRDLKPENVLLSSTS 331 ::: - ::: -	
DB	300 VLELMEGGELFKVGVNGKRLKEATCKLYFYOMLLAVOYLHENGIIHRDLKPENVLLSSQE 359 ::: - ::: -	
QY	332 BECCIKITDFGOSKILGETSLMRTLTCGTPTYLAPEVLNTAGTTGYSSAVDCWSLGVLV 391 ::: - ::: -	
DB	360 EDCLIKITDFGHSKILGETSLMRTLTCGTPTYLAPELVSVGTAGYNRAVDCWSLGVLFI 419 ::: - ::: -	
QY	392 CLCGYPPFSEQSNIPLNQIAEGKYTVIAAARNVSEQAFLVKNLLVVDPPEORLTQK 451 ::: - ::: -	
DB	420 CLUGYPPFSEHRTQVSLKDQITSGKYNFIPEVWAEVSEKALDLVKLLVVDPKARFTTEE 479 ::: - ::: -	
QY	452 ALEHPWLQDSMKHTVERLMYGVDHTMPPP---IKNIIRKRHEWDQDASTSS----C 503 ::: - ::: -	
DB	480 ALRHPWLQDEDWKRFQDLLSEENESTALPOVLAQPSTSRKRPRGEAGEATTTRKPAVC 539 ::: - ::: -	
QY	504 SEIL 507 : :	
DB	540 AAVL 543	
	RESULT 6 ABG30701 ID ABG30701 standard; protein; 543 AA. XX AC XX ABG30701; XX DT XX 07-OCT-2002 (first entry) XX Human checkpoint kinase 2 (CHK2) polypeptide. DE DE XX Human; checkpoint kinase 2; CHK2; enzyme; antisense therapy. XX OS Homo sapiens. XX PN WO200251858-A2.	

CC elevated expression of EDD protein in a cell; (11) an antisense nucleic acid, ribozyme, peptide nucleic acid (PNA), interfering RNA or siRNA; and (12) a pharmaceutical composition comprising the antisense nucleic acid, ribozyme, PNA, interfering RNA or siRNA. EDD has cytostatic activity, and can be used in gene therapy. The methods and modulator are useful for treating a condition associated with EDD over expression such as cancer, e.g. squamous cell carcinoma, hepatocellular carcinoma, ovarian cancer, breast cancer, melanoma, head and neck cancer, adenocarcinoma, squamous lung cancer, gastrointestinal cancer (e.g. gastric, colon, or pancreatic cancer), renal cell cancer, bladder cancer, prostate cancer, non-squamous carcinoma, glioblastoma and medullablastoma. The components and composition are useful for reducing the expression of EDD in a cell to inhibit cellular proliferation. The present sequence represents human Chk2 transcript variant 1 protein, which is used in the exemplification of the present invention.

XX Sequence 543 AA;

Query Match 61.0%; Score 1655.5; DB 8; Length 543;
Best Local Similarity 59.9%; Pred. No. 1.6e-147;
Matches 326; Conservative 74; Mismatches 105; Indels 39; Gaps 7;
QY 2 MSRDYTKTSQ-----QSGTSSSSSSAP-QSYSSSSSSGTL 37
DB 1 MSRESDEVAQSHGSSACSPHGSVTSQSGSSSQSGISSSTSTMPNSSQSHSSGTL 60
QY 38 SSDLTPVQDLASI-----PEDPEIDEDIPQWGLMALGKFLNHDCLHEEYVGRDKK 92
DB 61 SLETSTVSTQELYSIPEDQEPEDQEPPTAPWALMALQDGFANLECVNDNYWFGDRKS 120
QY 93 CDYTFDIPVLNQTDYKTYSKRHFIFQELGHGHSRVANIEDLSGNGTFVFNKEIIGKRT 152
DB 121 CEYCFDEPLLKRTDKYRTSKKHFRIFREVGPKNSYIAYIEDHSGNGTFVNTLVGKGR 180
QY 153 LPLTNNAIALSLPNKVFVFDLSVDQDTYKDFIDKYIMSRPIGSGACGEVKLAFQK 212
DB 181 RPLNNSBIALSLSRNKVFVFDLTVDQSVYPKALRDEYIMSKTLGSGACGEVKLAFER 240
QY 213 SVCKKVAVKIISKRFKNTSSNEHP-ISVDTEIILKLDHPDPIIKIENFDSDFYI 271
DB 241 KTKCKVAIKIISKRFKFAIGSAREADPALNVETEILKLNHPDPIIKIKNFDDAED-YII 299
QY 272 VLELMEGGELPDRVNVNSTRLEPIAKLYFYQMLLAVQYLHENGVIHRDLKPEVLLSSTS 331
DB 300 VLELMEGGELPKVGVGNKRLKEATCKLYFYQMLLAVQYLHENGIIHRDLKPEVLLSSQE 359
QY 332 BECCIKITDFGOSKILGETSLMRTLCTGPTTYLAPEVLNAGTTGYSSAVDCWSLGVILFV 391
DB 360 EDCLIKITDFGHSKILGETSLMRTLCTGPTTYLAPEVLVSVGTAGYNRAVDCWSLGVILFI 419
QY 392 CLCGYPPFSEQNSNIPLNQIAEGKYTYIAAARNVSEQAFDLVKNLLAVDPQRLTTKQ 451
DB 420 CLSGYPPFSEHRTQVSLKDKQTSKYNFIPEVMAEVSEKALDLVKKLLVDPKARFTTEE 479
QY 452 ALEHPWLQDQSGMKHTVVERLMYGVDMTPPP---IKKNIIRKRGHWDDQASTSS-----C 503
DB 480 ALRHPWLQDEDMKRFQDLSEENESTALPQVLAQPSISRKRPREGAEGATTKRPVAVC 539
QY 504 SEIL 507
DB 540 AAVL 543

RESULT 8

ADM72213
ID ADM72213 standard; protein; 543 AA.

AC ADM72213;

DT 17-JUN-2004 (first entry)

XX Human TASK108 polypeptide.

KW TASK; tumour-associated kinase; cytostatic; tumour antigen;
XX cell proliferative disorder; cancer; transgenic; human.
OS Homo sapiens.
XX WO2004024064-A2.
XX 25-MAR-2004.
XX 05-SEP-2003; 2003WO-US027894.
XX 11-SEP-2002; 2002US-0410166P.
XX (GETH) GENENTECH INC.
XX Desauvage FJ, Wood WI, Zhang Z;
XX WPI; 2004-282985/26.
XX N-PSDB; ADM72212.
XX New tumor-associated kinase nucleic acids and polypeptides, useful as hybridization probes for isolating full length TASK DNA, for generating transgenic animals, in chromosome identification, or for tissue typing.
XX Claim 12; SEQ ID NO 18; 163pp; English.
XX The invention relates to new isolated tumour-associated kinase (TASK) nucleic acid molecules and encoded polypeptides. Cytostatic. The antibody, oligopeptide or organic molecule that binds to the TASK polypeptide are useful for treating a mammal having a tumour comprising cells expressing the polypeptide. Antagonists of TASK are useful for treating or preventing a cell proliferative disorder (e.g. cancer) associated with increased expression or activity of TASK polypeptide. The TASK polynucleotides and polypeptides may be used as hybridization probes for isolating full length TASK DNA, for generating transgenic animals, in chromosome identification, or for tissue typing. The present sequence represents a human TASK polypeptide.
XX Sequence 543 AA;

Query Match 61.0%; Score 1655.5; DB 8; Length 543;
Best Local Similarity 59.9%; Pred. No. 1.6e-147;
Matches 326; Conservative 74; Mismatches 105; Indels 39; Gaps 7;
QY 2 MSRDYTKTSQ-----QSGTSSSSSSAP-QSYSSSSSSGTL 37
DB 1 MSRESDEVAQSHGSSACSPHGSVTSQSGSSSQSGISSSTSTMPNSSQSHSSGTL 60
QY 38 SSDLTPVQDLASI-----PEDPEIDEDIPQWGLMALGKFLNHDCLHEEYVGRDKK 92
DB 61 SLETSTVSTQELYSIPEDQEPEDQEPPTAPWALMALQDGFANLECVNDNYWFGDRKS 120
QY 93 CDYTFDIPVLNQTDYKTYSKRHFIFQELGHGHSRVANIEDLSGNGTFVFNKEIIGKRT 152
DB 121 CEYCFDEPLLKRTDKYRTSKKHFRIFREVGPKNSYIAYIEDHSGNGTFVNTLVGKGR 180
QY 153 LPLTNNAIALSLPNKVFVFDLSVDQDTYKDFIDKYIMSRPIGSGACGEVKLAFQK 212
DB 181 RPLNNSBIALSLSRNKVFVFDLTVDQSVYPKALRDEYIMSKTLGSGACGEVKLAFER 240
QY 213 SVCKKVAVKIISKRFKNTSSNEHP-ISVDTEIILKLDHPDPIIKIENFDSDFYI 271
DB 241 KTKCKVAIKIISKRFKFAIGSAREADPALNVETEILKLNHPDPIIKIKNFDDAED-YII 299
QY 272 VLELMEGGELPDRVNVNSTRLEPIAKLYFYQMLLAVQYLHENGVIHRDLKPEVLLSSTS 331
DB 300 VLELMEGGELPKVGVGNKRLKEATCKLYFYQMLLAVQYLHENGIIHRDLKPEVLLSSQE 359
QY 332 BECCIKITDFGOSKILGETSLMRTLCTGPTTYLAPEVLNAGTTGYSSAVDCWSLGVILFV 391
DB 360 EDCLIKITDFGHSKILGETSLMRTLCTGPTTYLAPEVLVSVGTAGYNRAVDCWSLGVILFI 419
QY 392 CLCGYPPFSEQNSNIPLNQIAEGKYTYIAAARNVSEQAFDLVKNLLAVDPQRLTTKQ 451

Db	420	CLSGYPPFSEHRTQVSLKDOIITSGKNFIPDEWAEVSEKALDLVKKLLVVDPKARFTTEE	479
Qy	452	ALBHPWLQDSMKHRTVERLMYGVDMTPPP---IKNNIIKRGHEWDQDASTSS-----C	503
Db	480	ALRHPWLQDEDMKRRKFDLLSEENESTALPQVLAQPSGSKRPREGEAGEAETTKRPVAVC	539
Qy	504	SEIL 507	
Db	540	AAVL 543	
RESULT 9			
ID	ADO44010	ADO44010 standard; protein; 543 AA.	
XX	AC	ADO44010;	
XX	DT	15-JUL-2004 (first entry)	
XX	XX	Amino acid sequence of human CHK2.	
DE	XX	protein complex; neurological disease; stroke; neurodegeneration;	
XX	KW	Wallerian degeneration; Alzheimer's disease; neurological disorder;	
KW	KW	epilepsy; inflammatory condition; ulcerative colitis; Crohn's disease;	
KW	KW	atherosclerosis; ID-MTO-inositol triphosphate 3 kinase A; ASK1; ASK2;	
KW	KW	ASK3; CaMKII beta; CaMKII delta; CaMKII gamma; casein kinase II alpha;	
KW	KW	Cdc37; CHK2; CTCL tumour antigen SE20-4; EF-1 alpha 1; EMAP;	
KW	KW	FLJ14653 NT2RP2002252; FLJ30839 FEBRA2002429; HERC2;	
KW	KW	inositol polyphosphate-5-phosphatase; inositol-1; 4;	
KW	KW	5-triphosphate 5-phosphatase type 1; IRAK1; IRAK4; KIAA1441; MSTP030;	
KW	KW	Nek9; PAR3; Pellino 1; Pellino 3; podocalyxin-like protein 1 precursor;	
KW	KW	Pushover; S-adenosylhomocysteine;	
KW	KW	secretory carrier-associated membrane protein 2; surfactant protein 2;	
KW	KW	ubiquitin carboxyl terminal hydrolase 11;	
KW	KW	upstream regulatory element binding protein 1; Vartul;	
KW	KW	Werner's syndrome helicase interacting protein; WHIP;	
KW	KW	X-ray repair cross complementing protein 4.	
XX	OS	Homo sapiens.	
XX	XX	WO2004031242-A2.	
XX	XX	15-APR-2004.	
XX	PF	11-SEP-2003; 2003WO-EP010110.	
XX	XX	12-SEP-2002; 2002EP-00020495.	
PR	PR	12-SEP-2002; 2002EP-00020496.	
PR	PR	12-SEP-2002; 2002EP-00020497.	
XX	XX	(CELL-) CELLZOME AG.	
PA	PA	Bouwmeester T, Drewes G, Jackson D, Helftenbein G, Schirle M;	
XX	PI	Kuester B, Hopf C;	
XX	XX	WPI; 2004-316467/29.	
XX	XX	New complex comprising at least one first protein, and at least one	
PT	PT	second protein, useful for treating stroke, Alzheimer's disease,	
PT	PT	neurological disorders such as epilepsy, and inflammatory conditions such	
PT	PT	as ulcerative colitis.	
XX	XX	Example; Page 246-248; 287pp; English.	
PS	PS	The specification describes protein complexes involved in cellular	
CC	CC	processes which have been shown to be critical for the development of	
CC	CC	various forms of neurological diseases. Three protein complexes were	
CC	CC	identified: ASK2 protein complex, Pellino-1 protein complex and Pellino-3	
CC	CC	protein complex. The protein complex are useful for treating diseases and	
CC	CC	disorders, e.g. stroke, neurodegeneration such as Wallerian degeneration,	
CC	CC	Alzheimer's disease, neurological disorders such as epilepsy, and	
CC	CC	inflammatory conditions such as ulcerative colitis, Crohn's disease or	
athrosclerosis. Proteins identified as being part of the protein			
complexes of the invention are ID-MYO-inositol triphosphate 3 kinase A,			
ASK1, ASK2, ASK3, CaMKII beta, CaMKII delta, CaMKII gamma, casein kinase			
II alpha, Cdc37, CHK2, CTCL tumour antigen SE20-4, EF-1 alpha 1, EMAP,			
FLJ14653 NT2RP2002252, FLJ30839 FEBRA2002429, HERC2, two hypothetical			
proteins of 35.5 kDa and 49.3 kDa, inositol polyphosphate-5-phosphatase,			
inositol-1,4,5-triphosphate 5-phosphatase type 1, IRAK1, IRAK4, KIAA1441,			
MSTP030, Nek9, PAR3, Pellino 1, Pellino 3, podocalyxin-like protein 1			
precursor, Pushover, a putative S-adenosylhomocysteine, secretory			
carrier-associated membrane protein 2, surfactant protein 2, ubiquitin			
carboxyl terminal hydrolase 11, upstream regulatory element binding			
protein 1, Vartul, Werner's syndrome helicase interacting protein (WHIP),			
X-ray repair cross complementing protein 4 (isoform 1). The present			
sequence represents CHK2.			
XX	XX	Sequence 543 AA;	
SQ	SQ	Query Match 61.0%; Score 1655.5; DB 8; Length 543;	
		Best Local Similarity 59.9%; Pred. No. 1.6e-147; Indels 39; Gaps 7;	
		Matches 326; Conservative 74; Mismatches 105;	
Qy	2	MSRDTKTESQ-----QSGTSSSSSSSSAP-QSYSSSSSGTL 37	
Db	1	MSRESDEVAQQSHGSSACSPHGSVTQSGSSSSQSGISSSTSTMPNSQSSSSGTL 60	
Qy	38	SLSDTVVPQDLASI-----PEPEDEIDIPQWGRMLWALGKGLNHDCLHEEYVDFDKK 92	
Db	61	SSLETVSTQELYSIPEDQEPDEPEETPPAWRLWALQDGFANLECVNDVYWFGRDKS 120	
Qy	93	CDYTDIPVLNCTDRKYTSKHFRIFOSLGHGSRVANIEDLSNGTGTVNEILCKGRT 152	
Db	121	CSYCFDEPLUKTKIRYTSKHFRIFEVGPNSYIAYIEDHSGNGTFTVTELGVGKR 180	
Qy	153	LPLTNNAETALSLPTNKVVFVSDLSVDDQTIYPKDFIDKYIMSRPTGSGACGEVKLAFQK 212	
Db	181	RLNNNSEIALSLSRKVFVFDLVDDQSVYPKALRDEYIMSKTLGSGACGEVKLAFER 240	
Qy	213	SVCKKVAVKIISKRFKMTSSNEHP-ISTDTEIELKLDHPICIIKENPFDSDFYI 271	
Db	241	KTCCKVAIKIISKRFKAIGSAREADPALNVETEIELKLDHPICIIKENPFDAED-VYI 299	
Qy	272	VLELMEGGELFDRVNVNSTRLEPIAKLYFYOMLAVQYLHENGVIHRDLKPENVLSSTS 331	
Db	300	VLELMEGGELFDKVVGNKRLKEATCKLYFYOMLAVQYLHENGVIHRDLKPENVLSSOE 359	
Qy	332	EECCIKITDFGQSKILGETSLMRTLCGTPYLAPEVLNATAGTGYSSAVDCWSLGVILFV 391	
Db	360	EDCLIKITDFGHSKILGETSLMRTLCGTPYLAPEVLNATAGTGYSSAVDCWSLGVILFI 419	
Qy	392	CLCGYPPFSEQNSNIPLNQIAEGKYTIAAARNVSEQAFDLVKNLLVVDPEQRUTTKQ 451	
Db	420	CLSGYPPFSEHRTQVSLKDOIITSGKNFIPDEWAEVSEKALDLVKKLLVVDPKARFTTEE 479	
Qy	452	ALEHPWLQDSMKHRTVERLMYGVDMTPPP---IKNNIIKRGHEWDQDASTSS-----C 503	
Db	480	ALRHPWLQDEDMKRRKFDLLSEENESTALPQVLAQPSGSKRPREGEAGEAETTKRPVAVC 539	
Qy	504	SEIL 507	
Db	540	AAVL 543	
RESULT 10			
ID	ADQ09232	ADQ09232 standard; protein; 543 AA.	
XX	AC	ADQ09232;	
XX	DT	23-SEP-2004 (first entry)	
XX	XX	Human CHK2 protein SEQ ID NO:417.	
XX	XX	thanatos-associated protein; THAP; THAP responsive gene; THAP family;	

THAP responsive element; angiogenesis; inflammation; metastasis; cancer; apoptosis; cardiovascular disease; neurodegenerative disease; chemokine; antiangiogenic; antiinflammatory; cardiovascular; cytostatic; neuroprotective; osteopathic; THAP modulator; THAP synthesis modulator; human.

Homo sapiens.

WO2004055050-A2.

01-JUL-2004

10-DEC-2003: 2003WO-TB006434

10-DEC-2002. 2003HC-0432699D

03-JUL-2003; 2003US-0485027P.

(ENDO-) ENDOCUBE SAS.

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N-PSDB; ADQ09233.

Modulating expres

comprises modulating the interaction of a THAP polypeptide with a nucleic acid.

Example 47; SEQ ID NO 417; 612pp; English.

The present invention describes a method for modulating the expression of a thymosin (death)-associated protein (THAP) responsive gene. The method comprises modulating the interaction of a THAP-family polypeptide or its biological fragment with a nucleic acid, and so enhancing or repressing the expression of the THAP responsive gene. Also described: (1) a method of modulating the expression of a gene responsive to a THAP/chemokine complex; (2) a pharmaceutical composition comprising a THAP responsive element in a pharmaceutical carrier; (3) a transcription factor decoy consisting essentially of a THAP responsive element; (4) a cell comprising a transcription factor decoy described above; (5) methods of modulating the interaction between a nucleic acid and a THAP-family polypeptide or its biological fragment, or a nucleic acid and a THAP/chemokine complex; (6) a vector packaging cell line comprising a cell comprising a viral vector which comprises a promoter operably linked to a nucleic acid encoding a THAP-family polypeptide or its biological fragment; (7) a method of constructing a cell which expresses a recombinant THAP-family polypeptide; (8) a method of ameliorating symptoms associated with a condition mediated by a THAP/chemokine complex; (9) methods of identifying a test compound that modulates transcription at a THAP responsive element or that modulates the transport of a chemokine into the nucleus; (10) methods for reducing the symptoms associated with a condition selected from excessive or insufficient angiogenesis, inflammation, metastasis of a cancerous tissue, excessive or insufficient apoptosis, cardiovascular disease and neurodegenerative diseases; symptoms associated with a condition resulting from the activity of a chemokine or a THAP-family polypeptide in an individual; or symptoms associated with transcriptional repression or activation mediated by a THAP-family polypeptide in an individual; (11) a vector comprising a THAP responsive promoter operably linked to a nucleic acid encoding a detectable product; (12) a genetically engineered cell comprising the vector described above or that expresses a THAP-family polypeptide or its biological fragment; (13) an in vitro transcription reaction comprising a nucleic acid comprising a THAP responsive promoter, ribonucleotides and an RNA polymerase; and (14) an isolated mutant THAP-family polypeptide that does not bind to a chemokine. The pharmaceutical composition has antiangiogenic, antiinflammatory, cardiovascular, cytostatic, neuroprotective and osteoprotective activities, and can be used for modulating the expression of a THAP responsive gene. Modulation can be used for reducing symptoms of conditions such as excessive or insufficient angiogenesis, inflammation, metastasis of a cancerous tissue, excessive

PA	(IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK.	phosphorylation; cancer; proliferative disease; cytostatic; gene therapy.
XX	WPI; 2002-145186/19.	
DR	N-PSDB; AAL44751.	
XX		
XX	New gene encoding a protein for inhibiting human Chk2 phosphoenzyme activity.	
PT		
XX		
PS	Disclosure; Page 27-30; 36pp; Japanese.	
XX		
CC	The present invention provides the protein and coding sequences of a human Chk2 phosphoenzyme inhibitor. The sequences can be used in the chemotherapy of cancers. The present sequence is a protein described in the exemplification of the invention	
XX		
SQ	Sequence 543 AA;	
<p>Query Match 60.9%; Score 1651.5; DB 5; Length 543;</p> <p>Best Local Similarity 59.7%; Pred. No. 3.8e-147;</p> <p>Matches 325; Conservative 75; Mismatches 105; Indels 39; Gaps 7;</p>		
QY	2 MSRDRTKTESQ-----QSQGTSSSSSSSAP-QSYQSSSSGTL 37	
DB	1 MSRESDEAQQSHGSSACSQPHGSVTQSQGSSSQSGISSTSTWPNSSQSHSSGTL 60	
QY	38 SSLDTVPVQDLASI-----PEDPEIDEDIPQWRLWALGKFLNHDCLHEEYVFGDKK 92	
DB	61 SLSLETSTOELYSIPEDQEPDEPPTAPWRLWALQDGFANLECVNDNYWFGDKS 120	
QY	93 CDYTFDIPVLNODRYKTYSKRHFRIFOELGHGHSRVANIEDLSGNGTFVNKEILGKRT 152	
DB	121 CEYCFDEPLLRKTRDYTSKGRHFRIFREVGPKNSYIAYIEDHSGNGTFVNTLVGKGR 180	
QY	153 LPLTNNAEIALSLPTNKVFVFSVDDQTIYPKDFIDKYIMSRPIGSGACGEVKLAFQ 212	
DB	181 RPLNNSEIALSLRNKVFVFDLTVDQSVYPKALRDEYVMSKTLGSGACGEVKLAF 240	
QY	213 SVCKKVAVKIISKRPKRNNTSSNEHP- ISVDTEILKLDHPICIIKIENFDSDFYI 271	
DB	241 KTCCKVAIKIISKRKFAIGSAREADPALNVETEILKLNHPICIIKKNFPAED-YYI 299	
QY	272 VLELMGGELFDRVNVNSTRLREPIAKLYFQMLLAVOYLHENGVIHRDLKPNVLLSST 331	
DB	300 VLELMGGELFDKVGNGKRLKEATCKLYFYQMLLAVOYLHENGIIHRDLKPNVLLSSE 359	
QY	332 EECIKITDFQSKILGETSLMRTLCGTPTYLAPELVNTAGTGYSSAVDCMSGLVILFV 391	
DB	360 EDCLIKITEFGHSHKILGETSLMRTLCGTPTYLAPELVSVGTAGYNRAVDCMSGLVILFI 419	
QY	392 CLCGYPPFPSEQNSNIPKQIAGKYTYIAAARNVSEQAFDLVKNLLVVDPEQLRTTKQ 451	
DB	420 CLSGYPPFSEHRTQVSLKQDITSGKYNFIPVWAEVSEKALDLVKKLLVVDPKARFTTE 479	
QY	452 ALRHPWLQDDSMKHTVERLMYGVHDHTMPP- --IKNNIIRKRGHEWDQDASTSS- ---C 503	
DB	480 ALRHPWLQDDMKRKFQDLLSEENESTALPQVLAQPSSTSRKRPREGEAETTKRPVAVC 539	
QY	504 SEIL 507	
DB	540 AAVL 543	
<p>RESULT 12</p> <p>AAV67968</p> <p>ID AAV67968 standard; protein; 543 AA.</p> <p>XX AAV67968;</p> <p>XX</p> <p>XX</p> <p>DT 05-APR-2000 (first entry)</p> <p>XX Human cell cycle regulatory factor Cds1 SEQ ID NO:1.</p> <p>DE Human; cell cycle regulatory factor; Cds1; hcds1; cdc25; histone H1;</p> <p>XX</p> <p>KW</p>		
KW	phosphorylation; cancer; proliferative disease; cytostatic; gene therapy.	
XX	Homo sapiens.	
OS		
XX	W09967369-A1.	
PN		
XX	29-DEC-1999.	
PD		
XX		
PF	23-JUN-1999; 99WO-JP003350.	
XX		
PR	23-JUN-1999; 98JP-00192467.	
XX		
PA	(CHUS) CHUGAI SEIYAKU KK.	
XX		
PI	Nakanishi M;	
XX		
DR	WPI; 2000-106292/09.	
DR	N-PSDB; AA257411.	
XX		
PT	Cell cycle regulatory factor-encoding gene for production recombinant proteins with kinase activity, used to develop drugs to treat cancers and proliferative diseases.	
PT		
XX		
PS	Claim 1; Page 35-39; 52pp; Japanese.	
XX		
CC	The present sequence represents the human cell cycle regulatory factor Cds1. The Cds1 nucleotide sequence can be used in gene therapy. Cds1 may be used to detect inhibitors of cell cycle regulatory factors which can be applied in the development of drugs for treating cancers and proliferative diseases. Cds1 is strongly expressed in the testis as well as other tissues. Cds1 can efficiently phosphorylate cdc25 and histone H1	
XX		
SQ	Sequence 543 AA;	
<p>Query Match 60.6%; Score 1643.5; DB 3; Length 543;</p> <p>Best Local Similarity 59.6%; Pred. No. 2.2e-146;</p> <p>Matches 325; Conservative 75; Mismatches 104; Indels 41; Gaps 8;</p>		
QY	2 MSRDRTKTESQ-----QSQGTSSSSSSSAPQSYQSS--SSGT 36	
DB	1 MSRESDEAQQSHGSSACSQPHGSVTQSQGSSSQSGISSTSTWPNSSQSHSSGTL 59	
QY	37 LSSLTVPVQDLASI-----PEDPEIDEDIPQWRLWALGKFLNHDCLHEEYVFGDK 91	
DB	60 LSSLETSTOELYSIPEDQEPDEPPTAPWRLWALQDGFANLECVNDNYWFGDK 119	
QY	92 KCDYTFDIPVLNODRYKTYSKRHFRIFOELGHGHSRVANIEDLSGNGTFVNKEILGKGR 151	
DB	120 SCEYCFDEPLLRKTRDYTSKGRHFRIFREVGPKNSYIAYIEDHSGNGTFVNTLVGKGR 179	
QY	152 TLPLTNNAEIALSLPTNKVFVFSVDDQTIYPKDFIDKYIMSRPIGSGACGEVKLAFQ 211	
DB	180 RPLNNSEIALSLRNKVFVFDLTVDQSVYPKALRDEYVMSKTLGSGACGEVKLAF 239	
QY	212 KSVCKKVAVKIISKRPKRNNTSSNEHP- ISVDTEILKLDHPICIIKIENFDSDFYI 270	
DB	240 RXTCKKVAIKIISKRKFAIGSAREADPALNVETEILKLNHPICIIKKNFPAED-YY 298	
QY	271 IVLELMGGELFDRVNVNSTRLREPIAKLYFQMLLAVOYLHENGVIHRDLKPNVLLSST 330	
DB	299 IVLELMGGELFDKVGNGKRLKEATCKLYFYQMLLAVOYLHENGIIHRDLKPNVLLSSQ 358	
QY	331 SEECIKITDFQSKILGETSLMRTLCGTPTYLAPELVNTAGTGYSSAVDCMSGLVILF 390	
DB	359 BEDCLIKITEFGHSHKILGETSLMRTLCGTPTYLAPELVSVGTAGYNRAVDCMSGLVILFI 418	
QY	391 VCLCGYPPFPSEQNSNIPKQIAGKYTYIAAARNVSEQAFDLVKNLLVVDPEQLRTTK 450	
DB	419 ICLSGYPPFSEHRTQVSLKQDITSGKYNFIPVWAEVSEKALDLVKKLLVVDPKARFTTE 478	
QY	451 QALEHPWLQDDSMKHTVERLMYGVHDHTMPP- --IKNNIIRKRGHEWDQDASTSS- --- 502	
DB	479 EALRHPWLQDDMKRKFQDLLSEENESTALPQVLAQPSSTSRKRPREGEAETTKRPVAVC 538	

QY 503 CSEIL 507
 Db 539 CAAVL 543

RESULT 13
 ADN61455
 ID ADN61455 standard; protein; 586 AA.
 AC ADN61455;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Human KPP-21 protein SEQ ID NO:21.
 XX
 KW human; kinase; phosphatase; enzyme; KPP; cytostatic;
 KW antiarteriosclerotic; anticonvulsant; nootropic; neuroprotective;
 KW cerebroprotective; anti-HIV; antiallergic; antiinflammatory;
 KW thymimetic; gene therapy; cell proliferative disorder; cancer;
 KW atherosclerosis; neurological disorder; epilepsy; Huntington's disease;
 KW stroke; immune disorder; inflammatory disorder; AIDS; allergy;
 KW developmental disorder; Hypothyroidism; Cushing's syndrome; infection.
 XX
 OS Homo sapiens.
 XX
 PN WO2004042022-A2.
 XX
 PD 21-MAY-2004.
 XX
 PF 30-OCT-2003; 2003WO-US034809.
 XX
 PR 01-NOV-2002; 2002US-0423226P.
 PR 15-NOV-2002; 2002US-0426713P.
 PR 26-NOV-2002; 2002US-0429766P.
 PR 11-FEB-2003; 2003US-0447043P.
 XX
 PA (INCY-) INCYTE CORP.
 XX
 PI Hafalia AJA, Lee S, Murage J, Swarnakar A, Chawla NK, Khare R;
 PI Elliott VS, Tran UK, Ramkumar J, Gururajan R, Baughn MR, Gletzen KJ;
 PI Yang YG, Chien D, Wang JT, Favero KD, Becha SD, Richardson TW;
 PI Jin P, Hawkins PR, Yue H, Lee EA, Marquis JP;
 XX
 DR WPI: 2004-390608/36.
 DR N-PSDB; ADN61511.
 XX
 PT New human kinases and phosphatases (KPP), useful for diagnosing, treating
 PT and preventing diseases or conditions associated with the aberrant KPP
 PT expression e.g. cancer, AIDS, epilepsy, or infections.
 XX
 PS Claim 1; SEQ ID NO 21; 320pp; English.
 XX
 CC The present sequence represents a human kinase and phosphatase protein
 CC designated KPP-21. Human KPP sequences have cytostatic,
 CC antiarteriosclerotic, anticonvulsant, nootropic, neuroprotective,
 CC cerebroprotective, anti-HIV, antiallergic, antiinflammatory and
 CC thymimetic activities, and can be used in gene therapy. The human KPP
 CC polypeptides and polynucleotides of the invention are useful in
 CC diagnosing, treating and preventing diseases or conditions associated
 CC with the decreased expression or overexpression of KPP, such as cell
 CC proliferative (e.g. cancer, atherosclerosis), neurological (e.g.
 CC epilepsy, Huntington's disease, stroke), immune/inflammatory (e.g. AIDS,
 CC allergies) and developmental (e.g. Hypothyroidism, Cushing's syndrome)
 CC disorders, or infections. They are also useful in assessing the effects
 CC of exogenous compounds on the expression of nucleic acid and amino acid
 CC sequences of KPP. The KPP sequences or their fragments are useful in
 CC screening compounds for effectiveness as agonist or antagonist of the
 CC polypeptides, or in altering the expression of the target polynucleotide
 CC and compounds that specifically bind to or modulate the activity of the
 CC polypeptide.
 XX
 SQ Sequence 586 AA;

Query Match 59.9%; Score 1624; DB 8; Length 586;
 Best Local Similarity 55.5%; Pred. No. 1.7e-144;
 Matches 326; Conservative 74; Mismatches 105; Indels 82; Gaps 8;

QY 2 MSRTKTESQ-----SQGTSSSSSSSAP-QSYSSSSSSTL 37
 Db 1 MSRESDVBAQQSHGSSACSPHGSVTSQSSSSSQGTSSTSTMPNSSQSSSSSTL 60
 QY 38 SSLLDTVPVQDLASI-----PEDPEIDEDIPOPWGLMALGKFLNHD----- 79
 Db 61 SSLETVTQELYSIPEDQEPDEPEPTPAWRLMALQDGFANLETESGHVTSQSDLEL 120
 QY 80 -----CLHEEYVFEGRDKCKDYTFDIIVLNQTDRYK 109
 Db 121 LLSDDPPASASQAGIRGVRHHPVCSLKCVDNMYWGRDKSEYCFDEPLLRKTDYR 180
 QY 110 TYSKRHPRIFOELGHGHSRVANIIDLSONGTFVKEIIGKGTPLTLTNAAIALSLPTNK 169
 Db 181 TYSKKHFRIPREVGPKNSYIAYIEDHSGNGTFTVNTLVGKRRRPLNNSBIALSLSRNK 240
 QY 170 VFVFSDLSDVDDQTIYPKDFIDKYIMSRPIGSGACGEVKLAFQKSVCKKVAKIISKRFK 229
 Db 241 VFVFFDLTVDDQSVYPKALRDEYIMSKTIGSGACGEVKLAFERKTKKVAKIISKRKPA 300
 QY 230 MNTSSNEHP-ISVDTEIEILKLDHPCCIIEENFFDSEDFYIIVLELMEGGELFDRVYNS 288
 Db 301 IGSAREADPALNVETEIEILKLNHPCCIIEKNFFDAED-YIIVLELMEGGELFDRVYNS 359
 QY 289 TRLREPTAKLYFYQMLLAVQYLHENGVIHRLKPEVLLSSTSECCIKITDPOSKILG 348
 Db 360 KRLKEATCKLYFYQMLLAVQYLHENGVIHRLKPEVLLSSTSECCIKITDPOSKILG 419
 QY 349 ETSLMRTLCTGPTYLAPVLTAGTGYSSAVDCWSLGVILFVCLCGYPPFSEQNINPL 408
 Db 420 ETSLMRTLCTGPTYLAPVLTAGTGYSSAVDCWSLGVILFVCLCGYPPFSEQNINPL 479
 QY 409 KNQIAEGKTYIAAAWRNVSEQAFDLVKNLLVVDPEQRLTTKQALEHPWLQDSDMKHTVE 468
 Db 480 KDQITSGKYNFIPEWAEVSEKALDLVKLLVVDPKARFTTEALRHPWLQDSDMKRKFQ 539
 QY 469 RLMTGVDMTHMPP-----IKNNIRKRHEWQDQASTSS-----CSEIL 507
 Db 540 DLLSENESTALPQVLAQPSTSRKRPRGEAGEAETTKRPAVCAVL 586

RESULT 14
 AAM48994
 ID AAM48994 standard; protein; 514 AA.
 XX
 AC AAM48994;
 XX
 DT 08-JUL-2002 (first entry)
 XX
 DE Human Chk2 phosphoenzyme inhibitor.
 XX
 KW Human; Chk2 phosphoenzyme inhibitor; cytostatic.
 XX
 OS Homo sapiens.
 XX
 PN JP2001346588-A.
 XX
 PD 18-DEC-2001.
 XX
 PF 08-JUN-2000; 2000JP-00172273.
 XX
 PR 08-JUN-2000; 2000JP-00172273.
 XX
 PA (IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK.
 XX
 DR WPI: 2002-145186/19.
 DR N-PSDB; AAL44749.
 XX

PT	New gene encoding a protein for inhibiting human Chk2 phosphoenzyme activity.																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																
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KW	prostate cancer; non-squamous carcinoma; glioblastoma; medullablastoma;	
XX	Chk2 transcript variant 2.	
XX	Homo sapiens.	
OS	WO2004022750-A1.	
PN	18-MAR-2004.	
XX		
XX	05-SEP-2003; 2003WO-AU001164.	
XX		
PR	05-SEP-2002; 2002AU-00951346.	
PR	07-NOV-2002; 2002US-0425218P.	
XX	(GARV-) GARVAN INST MEDICAL RES.	
PA	Watte C, Saunders D, Henderson M, Clancy J, Henshall S;	
PI	Sutherland R, O'Brien P;	
PI	WPI; 2004-248472/23.	
DR	N-PSDB; ADL32562.	
XX	Detecting a cancer cell in a subject sample, also related to cancer	
PT	treatments, comprises determining the level of nucleic acid that is	
PT	linked to map position 8q22.3 of the human genome or its expression	
PT	product.	
XX	Claim 29; SEQ ID NO 21; 331pp; English.	
PS	The present invention describes a method for detecting a cancer cell in a	
XX	subject, which comprises determining the level of nucleic acid that is	
CC	linked to map position 8q22.3 of the human genome or its expression	
CC	product in a sample of the subject, where an elevated level of the	
CC	nucleic acid or polypeptide is indicative of cancer in the subject. Also	
CC	described: (1) a method for diagnosing a cancer or predicting recurrence	
CC	of a cancer in a subject comprising determining the level of mRNA or	
CC	protein encoded by a nucleic acid as described above; (2) the isolated	
CC	nucleic acid molecule for detecting cancer cell; (3) an isolated or	
CC	recombinant protein complex; (4) an antibody that binds to the protein	
CC	complex; (5) a kit for detecting or producing a protein complex,	
CC	comprising an EDD polypeptide or a portion of an EDD polypeptide and a	
CC	second polypeptides selected from a protein having tumour suppressor	
CC	activity, a protein having cell cycle modulatory activity, a protein	
CC	associated with DNA repair or damage, a nuclear targeting protein, and a	
CC	progesterone receptor protein or its portion, where the portion of the	
CC	second polypeptide is sufficient to bind to the EDD polypeptide or the	
CC	portion of an EDD polypeptide; (6) methods for isolating the protein	
CC	complex; (7) a method for determining a predisposition for disease, or	
CC	disease state; (8) a method for determining a modulator of the activity,	
CC	formation or stability of an isolated or recombinant protein complex; (9)	
CC	a method for determining a modulator of the level of protein complex	
CC	formation; (10) a method for treating a condition associated with	
CC	elevated expression of EDD protein in a cell; (11) an antisense nucleic	
CC	acid, ribozyme, peptide nucleic acid (PNA), interfering RNA or siRNA; and	
CC	(12) a pharmaceutical composition comprising the antisense nucleic acid,	
CC	ribozyme, PNA, interfering RNA or siRNA. EDD has cytostatic activity, and	
CC	can be used in gene therapy. The methods and modulator are useful for	
CC	treating a condition associated with EDD over expression such as cancer,	
CC	e.g. squamous cell carcinoma, hepatocellular carcinoma, ovarian cancer,	
CC	breast cancer, melanoma, head and neck cancer, adenocarcinoma, squamous	
CC	lung cancer, gastrointestinal cancer (e.g. gastric, colon, or pancreatic	
CC	cancer), renal cell cancer, bladder cancer, prostate cancer, non-squamous	
CC	carcinoma, glioblastoma and medullablastoma. The components and	
CC	composition are useful for reducing the expression of EDD in a cell to	
CC	inhibit cellular proliferation. The present sequence represents human	
CC	Chk2 transcript variant 2 protein, which is used in the exemplification	
CC	of the present invention.	
XX	Sequence 514 AA;	
SQ	Query Match	
	Best Local Similarity 55.3%; Score 1499; DB 8; Length 514;	
	Matches 302; Conservative 72; Mismatches 102; Indels 68; Gaps 8;	

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 7, 2005, 12:56:39 ; Search time 163 Seconds
(without alignments)
1225.354 Million cell updates/sec

Title: US-10-618-173-2
Perfect score: 2712
Sequence: 1 MMSRDTKTESQSQGTSSSS.....ASTSSCSEILPTSAEKRAKR 517

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1726216 seqs, 386330316 residues
Total number of hits satisfying chosen parameters: 1726216

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications AA:*
- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
 - 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
 - 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
 - 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
 - 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
 - 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
 - 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
 - 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
 - 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
 - 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
 - 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
 - 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
 - 17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
 - 18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
 - 19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
 - 20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
 - 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
 - 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2712	100.0	517	9 US-09-849-617-2	Sequence 2, Appli
2	2712	100.0	517	15 US-10-618-173-2	Sequence 2, Appli
3	1655.5	61.0	543	14 US-10-185-182A-2	Sequence 2, Appli
4	1655.5	61.0	543	16 US-10-733-878-417	Sequence 417, App
5	1655.5	61.0	543	16 US-10-820-583A-2	Sequence 2, Appli
6	1644.5	60.6	545	14 US-10-142-356-6	Sequence 6, Appli
7	1643.5	60.6	543	9 US-09-740-627-1	Sequence 1, Appli
8	1499	55.3	514	16 US-10-820-583A-3	Sequence 3, Appli
9	1096.5	40.4	326	17 US-10-881-124A-9	Sequence 9, Appli
10	1096.5	40.4	327	17 US-10-881-124A-8	Sequence 8, Appli
11	836.5	30.8	459	9 US-09-740-627-9	Sequence 9, Appli

12	621	22.9	513	15	US-10-369-493-1578	Sequence 1578, Ap
13	603	22.2	356	10	US-09-733-388-4	Sequence 4, Appli
14	603	22.2	356	15	US-10-446-175-4	Sequence 4, Appli
15	603	22.2	356	17	US-10-936-445-4	Sequence 4, Appli
16	600.5	22.1	355	14	US-10-355-975-10	Sequence 10, Appli
17	600.5	22.1	355	15	US-10-258-106-11	Sequence 11, Appli
18	600.5	22.1	357	14	US-10-024-036B-2	Sequence 2, Appli
19	600.5	22.1	357	15	US-10-258-106-2	Sequence 2, Appli
20	600.5	22.1	357	16	US-10-737-450-2	Sequence 2, Appli
21	600.5	22.1	357	16	US-10-782-695-33	Sequence 33, Appli
22	600.5	22.1	385	10	US-09-733-388-2	Sequence 2, Appli
23	600.5	22.1	385	15	US-10-446-175-2	Sequence 2, Appli
24	600.5	22.1	385	17	US-10-936-445-2	Sequence 2, Appli
25	593.5	21.9	332	16	US-10-664-421-13	Sequence 13, Appli
26	591.5	21.8	317	10	US-09-935-464-36	Sequence 36, Appli
27	591.5	21.8	317	14	US-10-125-835-36	Sequence 36, Appli
28	591.5	21.8	326	16	US-10-664-421-55	Sequence 55, Appli
29	591.5	21.8	370	9	US-09-817-181-4	Sequence 4, Appli
30	591.5	21.8	370	10	US-09-769-970-19	Sequence 19, Appli
31	591.5	21.8	370	14	US-10-142-356-7	Sequence 7, Appli
32	591.5	21.8	370	14	US-10-300-828-4	Sequence 4, Appli
33	591.5	21.8	370	14	US-10-090-002-4	Sequence 4, Appli
34	591.5	21.8	370	14	US-10-204-041-10	Sequence 10, Appli
35	591.5	21.8	370	16	US-10-649-400-6	Sequence 6, Appli
36	591.5	21.8	370	16	US-10-740-835-5	Sequence 5, Appli
37	591.5	21.8	370	16	US-10-487-090-4	Sequence 4, Appli
38	580.5	21.4	460	10	US-09-935-464-3	Sequence 3, Appli
39	580.5	21.4	460	14	US-10-125-835-3	Sequence 3, Appli
40	580.5	21.4	476	9	US-09-960-643-2	Sequence 2, Appli
41	580.5	21.4	476	10	US-09-935-464-5	Sequence 5, Appli
42	580.5	21.4	476	14	US-10-125-835-5	Sequence 5, Appli
43	580.5	21.4	476	15	US-10-380-235-4	Sequence 4, Appli
44	575.5	21.2	522	9	US-09-740-627-11	Sequence 11, Appli
45	575.5	21.2	821	14	US-10-081-119-16	Sequence 16, Appli

ALIGNMENTS

RESULT 1
US-09-849-617-2
; Sequence 2, Application US/09849617
; Publication No. US20020086392A1
; GENERAL INFORMATION:
; APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY
; APPLICANT: GUO, Zijian
; APPLICANT: DUNPHY, William
; TITLE OF INVENTION: CHECKPOINT-ACTIVATING OLIGONUCLEOTIDES
; FILE REFERENCE: CITI350-1
; CURRENT APPLICATION NUMBER: US/09/849,617
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US 60/202,028
; PRIOR FILING DATE: 2000-05-04
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 517
; TYPE: PRT
; ORGANISM: Xenopus laevis
US-09-849-617-2

Query Match	100.0%;	Score 2712;	DB 9;	Length 517;
Best Local Similarity	100.0%;	Pred. No. 3.5e-193;		
Matches 517;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MMSRDTKTESQSQGTSSSSSSAPQSYSSQSSSSGTLSSLDTPVQDLASIPEDPEIDED 60		
Db	1	MMSRDTKTESQSQGTSSSSSSAPQSYSSQSSSSGTLSSLDTPVQDLASIPEDPEIDED 60		
Qy	61	IPQPMGRWLWALGKGFNLHNDCLHEEYVFGDKKCDYTFDIPVLNQTDRYKTKSRHFRIFQ 120		
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QY 121 ELGHSRVRANIEDLSGNGTFVNKEIIGKGRTPLTNNAEIALSLPTNKFVFSLSVDD 180
DB 121 ELGHSRVRANIEDLSGNGTFVNKEIIGKGRTPLTNNAEIALSLPTNKFVFSLSVDD 180
QY 181 QTIYPKDFIDKYIMSRPIGSGACGEVKLAFQSVCKKVAVKIISKRKFQNTSSNEHPIS 240
DB 181 QTIYPKDFIDKYIMSRPIGSGACGEVKLAFQSVCKKVAVKIISKRKFQNTSSNEHPIS 240
QY 241 VTEIEILKLDHPICIIKENFDFSEDFFYIVLELMEGGELFDRVNVNSTRLEPIAKLYF 300
DB 241 VTEIEILKLDHPICIIKENFDFSEDFFYIVLELMEGGELFDRVNVNSTRLEPIAKLYF 300
QY 301 YQMLLAVOYLHENGVIHRDLKPEENVLLSSTSECCIKITDFQSKILGETSLMRTLCTGP 360
DB 301 YQMLLAVOYLHENGVIHRDLKPEENVLLSSTSECCIKITDFQSKILGETSLMRTLCTGP 360
QY 361 TYLAPEVLNTAGTTGYSSAVDCWSLGVILFVCLCGYPPFPSEQNSNIPLNQIAEGKYIYI 420
DB 361 TYLAPEVLNTAGTTGYSSAVDCWSLGVILFVCLCGYPPFPSEQNSNIPLNQIAEGKYIYI 420
QY 421 AAARNVSEQAFDLVKNLLVDPPEORLTTKQALEHPWLQDDSMKHTVERLMYGVVDHTMPP 480
DB 421 AAARNVSEQAFDLVKNLLVDPPEORLTTKQALEHPWLQDDSMKHTVERLMYGVVDHTMPP 480
QY 481 PIKNIIRKRGHEWDQDASTSSCSSEILPTSAEKRAKR 517
DB 481 PIKNIIRKRGHEWDQDASTSSCSSEILPTSAEKRAKR 517

RESULT 2

US-10-618-173-2
; Sequence 2, Application US/10618173
; Publication No. US20040018603A1
; GENERAL INFORMATION:
; APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY
; APPLICANT: GUO, Zijian
; APPLICANT: DUNPHY, William
; FILE OF INVENTION: CHECKPOINT-ACTIVATING OLIGONUCLEOTIDES
; FILE REFERENCE: CITI350-1
; CURRENT APPLICATION NUMBER: US/10/618,173
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: US/09/849,617
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US 60/202,028
; PRIOR FILING DATE: 2000-05-04
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 517
; TYPE: PRT
; ORGANISM: Xenopus laevis
US-10-618-173-2

Query Match 100.0%; Score 2712; DB 15; Length 517;
Best Local Similarity 100.0%; Pred. No. 3.5e-193;
Matches 517; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMSRDTKTESQSQGCTSSSSSSAPQSYQSSSGTSLSLDTPVPQDLASIPEDPEIDED 60
DB 1 MMSRDTKTESQSQGCTSSSSSSAPQSYQSSSGTSLSLDTPVPQDLASIPEDPEIDED 60
QY 61 IFQPWGRWLWALGKFLNHDCLHEEYVFGDKKCDYTFDIPVLNQTDRYKTSKRHFRIQ 120
DB 61 IFQPWGRWLWALGKFLNHDCLHEEYVFGDKKCDYTFDIPVLNQTDRYKTSKRHFRIQ 120
QY 121 ELGHSRVRANIEDLSGNGTFVNKEIIGKGRTPLTNNAEIALSLPTNKFVFSLSVDD 180
DB 121 ELGHSRVRANIEDLSGNGTFVNKEIIGKGRTPLTNNAEIALSLPTNKFVFSLSVDD 180
QY 181 QTIYPKDFIDKYIMSRPIGSGACGEVKLAFQSVCKKVAVKIISKRKFQNTSSNEHPIS 240
DB 181 QTIYPKDFIDKYIMSRPIGSGACGEVKLAFQSVCKKVAVKIISKRKFQNTSSNEHPIS 240

QY 241 VTEIEILKLDHPICIIKENFDFSEDFFYIVLELMEGGELFDRVNVNSTRLEPIAKLYF 300
DB 241 VTEIEILKLDHPICIIKENFDFSEDFFYIVLELMEGGELFDRVNVNSTRLEPIAKLYF 300
QY 301 YQMLLAVOYLHENGVIHRDLKPEENVLLSSTSECCIKITDFQSKILGETSLMRTLCTGP 360
DB 301 YQMLLAVOYLHENGVIHRDLKPEENVLLSSTSECCIKITDFQSKILGETSLMRTLCTGP 360
QY 361 TYLAPEVLNTAGTTGYSSAVDCWSLGVILFVCLCGYPPFPSEQNSNIPLNQIAEGKYIYI 420
DB 361 TYLAPEVLNTAGTTGYSSAVDCWSLGVILFVCLCGYPPFPSEQNSNIPLNQIAEGKYIYI 420
QY 421 AAARNVSEQAFDLVKNLLVDPPEORLTTKQALEHPWLQDDSMKHTVERLMYGVVDHTMPP 480
DB 421 AAARNVSEQAFDLVKNLLVDPPEORLTTKQALEHPWLQDDSMKHTVERLMYGVVDHTMPP 480
QY 481 PIKNIIRKRGHEWDQDASTSSCSSEILPTSAEKRAKR 517
DB 481 PIKNIIRKRGHEWDQDASTSSCSSEILPTSAEKRAKR 517

RESULT 3

US-10-185-182A-2
; Sequence 2, Application US/10185182A
; Publication No. US20030017160A1
; GENERAL INFORMATION:
; APPLICANT: LUYTEN, Walter H.M.L.
; APPLICANT: PARKER, Andrew E.
; APPLICANT: MCGOWAN, Clare H.
; APPLICANT: BLASINA, Alessandra
; TITLE OF INVENTION: HUMAN CHECKPOINT KINASE, hCDS1,
; FILE OF INVENTION: COMPOSITIONS AND METHODS
; FILE REFERENCE: TSRI 649.0 Div.1
; CURRENT APPLICATION NUMBER: US/10/185,182A
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: US 09/529,093
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: PCT/EP98/06981
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: GB 9722320.0
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 543
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-185-182A-2

Query Match 61.0%; Score 1655.5; DB 14; Length 543;
Best Local Similarity 59.9%; Pred. No. 1.5e-114;
Matches 326; Conservative 74; Mismatches 105; Indels 39; Gaps 7;

QY 2 MSRDTKTESQ-----QQGTSSSSSSSAP-QSYQSSSSSGTL 37
DB 1 MSRESDEVAQSHGSSSACQPHGVSVTQSGSSSQSGISSTSTMPNSSQSSSSGTL 60
QY 38 SSLDTPVPQDLASI-----PEDPEIDEDIPOPWGRWLWALGKFLNHDCLHEEYVFGDKK 92
DB 61 SLETVTSTQELYSIPEDQPEEPTTPAWKLMALQDGFANLECVDNDYWTGRDKS 120
QY 93 CDYTPDIPVLNQTDRYKTSKRHFRIQELGHSRVRANIEDLSGNGTFVNKEIIGKRT 152
DB 121 CEYCFDEPLLKRTDKYRTYSKKGFRIFREVGPKNYSIAVIEDHSGNGTFVNTELVGKGR 180
QY 153 LPLTNNAEIALSLPTNKFVFSLSVDDQTYPKDFIDKYIMSRPIGSGACGEVKLAFQ 212
DB 181 RPLNNSBIALSLSNKVFVFFDLTVDDQSVYPKALRDEYIMSKTIGSGACGEVKLAF 240
QY 213 SVCKKVAVKIISKRKFQNTSSNEHP-ISVDTEIEILKLDHPICIIKENFDFSEDFFYI 271
DB 241 KTCKKVAVKIISKRKFQNTSSNEHP-IPALNVETEIEILKLDHPICIIKENFDFDAED-YYI 299

QY 272 VLEMEGGELFDRVNSTRLREPIAKLYFYQMLLAVOYLHENGVIHRDLKPNVLLSSTS 331
Db 300 VLEMEGGELFDRVNGKRLKEATCKLYFYQMLLAVOYLHENGIIHRDLKPNVLLSSQE 359
QY 332 EECCKITDFGQSKILGETSLMRTLCTGPTYLAPEVLNTAGTGYSSAVDCWSLGVILFV 391
Db 360 EDCLIKITDFGHSKILGETSLMRTLCTGPTYLAPEVLVSVGTAGYNRAVDCWSLGVILFI 419
QY 392 CLCGYPPFSEQNSNIPLNQIABGKTYIAAARNVSEQAFDLVKNLLVVDPEQRITTKQ 451
Db 420 CLSGYPPFSEHRTQVSLKDQITSGKYNFPEVMAEVSSEKALDLVKLLVVDPKARFTTEE 479
QY 452 ALEHPWLQDDSMKHTVERLMYGVHDHTMPPP---IKNNIRKRGHEWDQDASTSS---C 503
Db 480 ALRHPWLQDDMKRKFQDLLSEENESTALPQVLAQPSRKPRGEAGEAETTKRPVAVC 539
QY 504 SEIL 507
Db 540 AAVL 543

RESULT 4

US-10-733-878-417
; Sequence 417, Application US/10733878
; Publication No. US20040224408A1
; GENERAL INFORMATION:
; APPLICANT: Jean-Philippe Girard
; APPLICANT: Francois Amalric
; APPLICANT: Myriam Roussigne
; APPLICANT: Thomas Clouaire
; TITLE OF INVENTION: THAP PROTEINS AS NUCLEAR RECEPTORS FOR
; TITLE OF INVENTION: CHEMOKINES AND ROLES IN TRANSCRIPTIONAL REGULATION, CELL
; FILE OF INVENTION: PROLIFERATION AND CELL DIFFERENTIATION
; FILE REFERENCE: BIOSANK.012A
; CURRENT APPLICATION NUMBER: US/10/733,878
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 60/432699
; PRIOR FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: 60/485027
; PRIOR FILING DATE: 2003-07-03
; NUMBER OF SEQ ID NOS: 535
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 417
; LENGTH: 543
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-733-878-417

Query Match 61.0%; Score 1655.5; DB 16; Length 543;
Best Local Similarity 59.9%; Pred. No. 1.5e-114;
Matches 326; Conservative 74; Mismatches 105; Indels 39; Gaps 7;
QY 2 MSRDTKTESQ-----QSQGTSSSSSSSAP-QSYSSSSSGTL 37
Db 1 MSRESDEVAQSHGSSACSPHGSVTSQSSSSSQSGISSSTSTMPNSSQSHSSGTL 60
QY 38 SSLDTVPVQDLASI-----PEDPEIDEDIPQWGRMLWALGKFLNHDCLHEEYVFGDRKK 92
Db 61 SLETVSTQELYSIPEDQEPEDQEPPTAPARLWALQDGFANLECVNDYVWFGDRKS 120
QY 93 CDYTFDIPVLNQTRDYKTYSKRHFRIFQELGHGHSRVANIEDLSGNGTFVNKEIIQKGR 152
Db 121 CEYCFDEPLKRTDKYRTYSKHHFRIFREVGPKNSIAYIEDSHGNGTFVNTLVGKGR 180
QY 153 LPLTNNAEIALSLPTNKKVVFSDLSVDDDTIYPKDFIDKYIMSRPTGSGACGEVKLAFQ 212
Db 181 RPLNNSEIALSLSRNKVVFVFDLTVDQSVTPKALRDEYIMSKTIGSGACGEVKLAF 240
QY 93 CDYTFDIPVLNQTRDYKTYSKRHFRIFQELGHGHSRVANIEDLSGNGTFVNKEIIQKGR 152
Db 121 CEYCFDEPLKRTDKYRTYSKHHFRIFREVGPKNSIAYIEDSHGNGTFVNTLVGKGR 180
QY 153 LPLTNNAEIALSLPTNKKVVFSDLSVDDDTIYPKDFIDKYIMSRPTGSGACGEVKLAFQ 212
Db 181 RPLNNSEIALSLSRNKVVFVFDLTVDQSVTPKALRDEYIMSKTIGSGACGEVKLAF 240
QY 213 SVCKKVAVKIISKRRKFMNTSSNEHP-ISVDTEIELKLDHPCTIIEKFDSDFYII 271
Db 241 KTCKKVAIKIISKRRKFAIGSAREADPALNVETEIELKLNHECTIIEKNFFDAED-YVI 299
QY 272 VLEMEGGELFDRVNSTRLREPIAKLYFYQMLLAVOYLHENGVIHRDLKPNVLLSSTS 331

Db 300 VLEMEGGELFDRVNGKRLKEATCKLYFYQMLLAVOYLHENGIIHRDLKPNVLLSSQE 359
QY 332 EECCKITDFGQSKILGETSLMRTLCTGPTYLAPEVLNTAGTGYSSAVDCWSLGVILFV 391
Db 360 EDCLIKITDFGHSKILGETSLMRTLCTGPTYLAPEVLVSVGTAGYNRAVDCWSLGVILFI 419
QY 392 CLCGYPPFSEQNSNIPLNQIABGKTYIAAARNVSEQAFDLVKNLLVVDPEQRITTKQ 451
Db 420 CLSGYPPFSEHRTQVSLKDQITSGKYNFPEVMAEVSSEKALDLVKLLVVDPKARFTTEE 479
QY 452 ALEHPWLQDDSMKHTVERLMYGVHDHTMPPP---IKNNIRKRGHEWDQDASTSS---C 503
Db 480 ALRHPWLQDDMKRKFQDLLSEENESTALPQVLAQPSRKPRGEAGEAETTKRPVAVC 539
QY 504 SEIL 507
Db 540 AAVL 543

RESULT 5

US-10-820-583A-2
; Sequence 2, Application US/10820583A
; Publication No. US20040242461A1
; GENERAL INFORMATION:
; APPLICANT: Schneider, Michael
; APPLICANT: Oh, Hidemasa
; TITLE OF INVENTION: Modulators of Telomere Stability
; FILE REFERENCE: HO-P02673US1
; CURRENT APPLICATION NUMBER: US/10/820,583A
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 60/461,095
; PRIOR FILING DATE: 2003-04-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 543
; TYPE: PRT
; ORGANISM: Human
US-10-820-583A-2

Query Match 61.0%; Score 1655.5; DB 16; Length 543;
Best Local Similarity 59.9%; Pred. No. 1.5e-114;
Matches 326; Conservative 74; Mismatches 105; Indels 39; Gaps 7;
QY 2 MSRDTKTESQ-----QSQGTSSSSSSSAP-QSYSSSSSGTL 37
Db 1 MSRESDEVAQSHGSSACSPHGSVTSQSSSSSQSGISSSTSTMPNSSQSHSSGTL 60
QY 38 SSLDTVPVQDLASI-----PEDPEIDEDIPQWGRMLWALGKFLNHDCLHEEYVFGDRKK 92
Db 61 SLETVSTQELYSIPEDQEPEDQEPPTAPARLWALQDGFANLECVNDYVWFGDRKS 120
QY 93 CDYTFDIPVLNQTRDYKTYSKRHFRIFQELGHGHSRVANIEDLSGNGTFVNKEIIQKGR 152
Db 121 CEYCFDEPLKRTDKYRTYSKHHFRIFREVGPKNSIAYIEDSHGNGTFVNTLVGKGR 180
QY 153 LPLTNNAEIALSLPTNKKVVFSDLSVDDDTIYPKDFIDKYIMSRPTGSGACGEVKLAFQ 212
Db 181 RPLNNSEIALSLSRNKVVFVFDLTVDQSVTPKALRDEYIMSKTIGSGACGEVKLAF 240
QY 213 SVCKKVAVKIISKRRKFMNTSSNEHP-ISVDTEIELKLDHPCTIIEKFDSDFYII 271
Db 241 KTCKKVAIKIISKRRKFAIGSAREADPALNVETEIELKLNHECTIIEKNFFDAED-YVI 299
QY 272 VLEMEGGELFDRVNSTRLREPIAKLYFYQMLLAVOYLHENGVIHRDLKPNVLLSSTS 331
Db 300 VLEMEGGELFDRVNGKRLKEATCKLYFYQMLLAVOYLHENGIIHRDLKPNVLLSSQE 359
QY 332 EECCKITDFGQSKILGETSLMRTLCTGPTYLAPEVLNTAGTGYSSAVDCWSLGVILFV 391
Db 360 EDCLIKITDFGHSKILGETSLMRTLCTGPTYLAPEVLVSVGTAGYNRAVDCWSLGVILFI 419


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; GENERAL INFORMATION:
; APPLICANT: Schneider, Michael
; TITLE OF INVENTION: Modulators of Telomere Stability
; FILE REFERENCE: HO-P02673US1
; CURRENT APPLICATION NUMBER: US/10/820,583A
; PRIOR FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 60/461,095
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 514
; TYPE: PRT
; ORGANISM: Human
US-10-820-583A-3

Query Match      55.3%; Score 1499; DB 16; Length 514;
Best Local Similarity 55.5%; Pred. No. 6e-103;
Matches 302; Conservative 72; Mismatches 102; Indels 68; Gaps 8;

QY 2 MSRDYKTESQ-----QSGTSSSSSSSAP-QSYSSSSSGTL 37
DB 1 MSRESDEVAQSHGSSACSQPHGVTQSGSSSQSGISSSTSTMPNSSQSSHSSGTL 60
QY 38 SSDLTVVQDLASI-----PEDEIDEDIPQWGRIMWALGKGLNHDCLHBEYVFGROKK 92
DB 61 SSLETVSTQELYSIPEDQPEDEPEPTPAWRLWALQDGFANLECVNDVNWFGROKS 120
QY 93 CDYTDIPVLOTDRYKTKYSKHFRIQELGHGHSRVANIEDLSNGTFFVKNKEIIGKRT 152
DB 121 CRYCFDEPLLRKTRDYRTYSKHFRIQELGHGHSRVANIEDLSNGTFFVKNKEIIGKRT 180
QY 153 LPLTNNAETALSPTNKNVVFSDLSVDDOTIYPKDFIDKYIMSRPTGSGACGEVKLAFOK 212
DB 181 RLNNNSEIALSLSRNKVVFDFDLTVDQSVVPKALRDEYIMSKTIGSGACGEVKLAFER 240
QY 213 SVCKVAVKIIISKRKPKMNTSNEHP-ISVDTEIELKKLDHPCIIKIENFPDSEDFYI 271
DB 241 KTCKKVAIKIISKRKFAIGSAREADPALNVETEIELKKLHPCIIKIKNPFDAD-YVI 299
QY 272 VLELMEGGELFDRVNSTLRPIAKLYEOMLLAVOYLHENGVIHRLDKPENVLSSSTS 331
DB 300 VLELMEGGELFDRVNSTLRPIAKLYEOMLLAVOYLHENGVIHRLDKPENVLSSSTS 336
QY 332 EECCIKITDQSGKILGETSLMRTLCGTPTYLAPEVLNTAGTGYSSAVDCMSLGVILFV 391
DB 337 -----ITDFGSKILGETSLMRTLCGTPTYLAPEVLNTAGTGYSSAVDCMSLGVILFV 390
QY 392 CLCGYPPFSEQNSNIPKLNQIAEGKYTYIAAAWRNVSEQAFDLVKNLLVVDPEQLRTTKQ 451
DB 391 CLSGYPPFSEHRTQVSLKDQITSGKYNFPEVMAEVSEKALDLVKKLLVVDPKARFTTEE 450
QY 452 ALEHPLQDSSMKHTVERLMYGVHDHTMPP----IKNNIIRKRGHEWDQDASTSS-----C 503
DB 451 ALRHPWLODEMKRKFQDLLENSESTALPQVLAQPSSTSRKRPREGEAETTKRPAYC 510
QY 504 SEITL 507
DB 511 AAVL 514

RESULT 9
US-10-881-124A-9
; Sequence 9, Application US/10881124A
; Publication No. US20050112746A1
; GENERAL INFORMATION:
; APPLICANT: Structural Genomix, Inc.
; APPLICANT: Antonysam, Stephen S.
; APPLICANT: Hendle, Jorg
; APPLICANT: Louis, Gordon V.
; TITLE OF INVENTION: Crystals and Structures of Protein Kinase CHK2
; FILE REFERENCE: 022132-001210US
; CURRENT APPLICATION NUMBER: US/10/881,124A
; CURRENT FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: US 60/484,389
; PRIOR FILING DATE: 2003-07-01
; PRIOR APPLICATION NUMBER: US 60/509,781
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Predicted sequence of CHK2KD expressed protein
; NAME/KEY: misc_feature
; OTHER INFORMATION: serine at position 1 is phosphorylated

; CURRENT APPLICATION NUMBER: US/10/881,124A
; CURRENT FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: US 60/484,389
; PRIOR FILING DATE: 2003-07-01
; PRIOR APPLICATION NUMBER: US 60/509,781
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-881-124A-9

Query Match      40.4%; Score 1096.5; DB 17; Length 326;
Best Local Similarity 64.8%; Pred. No. 3e-73;
Matches 210; Conservative 43; Mismatches 66; Indels 5; Gaps 3;

QY 180 DOTYPKDFIDKYIMSRPIGSGACGEVKLAFQSKVAVKIIISKRKPKMNTSNEHP- 238
DB 3 DQSVVPKALRDEYIMSKTIGSGACGEVKLAFERKTKKVAIKIISKRKFAIGSAREADPA 62
QY 239 ISVDTEIELKKLDHPCIIKIENFPDSEDFYIVLELMEGGELFDRVNSTLRPIAKL 298
DB 63 LNVETEIELKKLHPCIIKIKNPFDAD-YVI VLELMEGGELFDRVNSTLRPIAKL 121
QY 299 YFYOMLLAVOYLHENGVIHRLDKPENVLSSSTSSECCIKITDQSGKILGETSLMRTLCG 358
DB 122 YFYOMLLAVOYLHENGVIHRLDKPENVLSSQEECLIKITDQSGKILGETSLMRTLCG 181
QY 359 TPTYLAPEVLNTAGTGYSSAVDCMSLGVILFVCLCGYPPFSEQNSNIPKLNQIAEGKYT 418
DB 182 DPTYLAPEVLNTAGTGYSSAVDCMSLGVILFVCLCGYPPFSEHRTQVSLKDQITSGKN 241
QY 419 YIAAAWRNVSEQAFDLVKNLLVVDPEQLRTTKQALEHPLQDSSMKHTVERLMYGVHDHTM 478
DB 242 FIPEVMAEVSEKALDLVKKLLVVDPKARFTTEEALRHPWLODEMKRKFQDLLENSEST 301
QY 479 PPP----IKNNIIRKRGHEWDQDAS 499
DB 302 ALPQVLAQPSSTSRKRPREGEAEGA 325

RESULT 10
US-10-881-124A-8
; Sequence 8, Application US/10881124A
; Publication No. US20050112746A1
; GENERAL INFORMATION:
; APPLICANT: Structural Genomix, Inc.
; APPLICANT: Antonysam, Stephen S.
; APPLICANT: Hendle, Jorg
; APPLICANT: Louis, Gordon V.
; TITLE OF INVENTION: Crystals and Structures of Protein Kinase CHK2
; FILE REFERENCE: 022132-001210US
; CURRENT APPLICATION NUMBER: US/10/881,124A
; CURRENT FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: US 60/484,389
; PRIOR FILING DATE: 2003-07-01
; PRIOR APPLICATION NUMBER: US 60/509,781
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Predicted sequence of CHK2KD expressed protein
; NAME/KEY: misc_feature
; OTHER INFORMATION: serine at position 1 is phosphorylated
```



```

QY 380 VDCWSLGVILFVCLCGVPPPEQNSNIPKNOIAEGKYTYIAAARNVSEQAFDLVKNLL 439
Db 402 VDLWSAGVILFVCLCGVPPPEQNSNIPKNOIAEGKYTYIAAARNVSEQAFDLVKNLL 461
QY 440 VVDPEQLRTTKQALEHPWLQD-----DSMKHTVERLMYGVDDHTMP 479
Db 462 VLNPDERYNIDEALNHPWFNDIQQSSVSLEQLRLQI-TDNKIP 504

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RESULT 13

```

US-09-733-388-4
; Sequence 4, Application US/09733388
; Publication No. US2003006495A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Greg
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Abuin, Alejandro
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 602698el Human Kinase Proteins and
; FILE REFERENCE: Polynucleotides Encoding the Same
; CURRENT APPLICATION NUMBER: US/09/733,388
; CURRENT FILING DATE: 2000-12-07
; PRIOR FILING DATE: 2000-12-07
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-733-388-4

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Query Match 22.2%; Score 603; DB 10; Length 356;
Best Local Similarity 38.1%; Pred. No. 1.7e-36;
Matches 128; Conservative 62; Mismatches 106; Indels 40; Gaps 6;

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```

QY 198 IGSAGCEGVKLAFOKSVCKKAVAKIISKRFKMTSSNEHPIISVDTEILKKLDHPCII 257
Db 29 LGTGFSEVVLAEKATGKLFVAKCIPKALKGKES-----SIENEIAVLRRKHENIV 82
QY 258 KIENFDSDFYIVLELMEGGELFDRVNVNSTRLREPIAKLYFYQMLLAVQVYLHENGVIH 317
Db 83 ALEDIYESPNHLYLVQVLSGGELFDRIVEKGFYTEKDASTLIRQVLDVAVYLLHRMGIVH 142
QY 318 RDLKPNVLLSSTSECCIKITDFGQSKILGETSLMRTLCGTPTYLAPEVLNAGTTGYS 377
Db 143 RDLKPNLLYYSODEESKIMISDFGLSKWEGKGDVNSTAGTGGYVAPEVL---AQKPY 199
QY 378 SAVDCWSLGVILFVCLCGVPPPEQNSNIPKNOIAEGKYTYIAAARNVSEQAFDLVKN 437
Db 200 KAVDCWSIGVIAVILCGVPPFYDENDS-KLFEQILKAIEYFDPSPYWDIDISAKDFIRN 258
QY 438 LLVVDPEQLRTTKQALEHPWLQDSSMKHTVERLMYGVDDHTMPPIKKNIRKRGHEWQD- 496
Db 259 LMEKDPNKRYTCQAAHPHPIADTALNKNH-----ESVSAQIRKNFAKSK---WRQA 308
QY 497 -----DASTSSCSEILPTSAEK 513
Db 309 FNATAVVRHMRKHLGSSLDSSNASVSSSLASQK 344

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RESULT 14

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US-10-446-175-4
; Sequence 4, Application US/10446175
; Publication No. US2004001412A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Greg
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.

```

```

; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Abuin, Alejandro
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. US2004001412A1el Human Kinase Proteins and
; FILE REFERENCE: Polynucleotides Encoding the Same
; CURRENT APPLICATION NUMBER: US/10/446,175
; CURRENT FILING DATE: 2003-05-27
; PRIOR FILING DATE: US/09/733,388
; PRIOR FILING DATE: 2000-12-07
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-446-175-4

Query Match 22.2%; Score 603; DB 15; Length 356;
Best Local Similarity 38.1%; Pred. No. 1.7e-36;
Matches 128; Conservative 62; Mismatches 106; Indels 40; Gaps 6;

QY 198 IGSAGCEGVKLAFOKSVCKKAVAKIISKRFKMTSSNEHPIISVDTEILKKLDHPCII 257
Db 29 LGTGFSEVVLAEKATGKLFVAKCIPKALKGKES-----SIENEIAVLRRKHENIV 82
QY 258 KIENFDSDFYIVLELMEGGELFDRVNVNSTRLREPIAKLYFYQMLLAVQVYLHENGVIH 317
Db 83 ALEDIYESPNHLYLVQVLSGGELFDRIVEKGFYTEKDASTLIRQVLDVAVYLLHRMGIVH 142
QY 318 RDLKPNVLLSSTSECCIKITDFGQSKILGETSLMRTLCGTPTYLAPEVLNAGTTGYS 377
Db 143 RDLKPNLLYYSODEESKIMISDFGLSKWEGKGDVNSTAGTGGYVAPEVL---AQKPY 199
QY 378 SAVDCWSLGVILFVCLCGVPPPEQNSNIPKNOIAEGKYTYIAAARNVSEQAFDLVKN 437
Db 200 KAVDCWSIGVIAVILCGVPPFYDENDS-KLFEQILKAIEYFDPSPYWDIDISAKDFIRN 258
QY 438 LLVVDPEQLRTTKQALEHPWLQDSSMKHTVERLMYGVDDHTMPPIKKNIRKRGHEWQD- 496
Db 259 LMEKDPNKRYTCQAAHPHPIADTALNKNH-----ESVSAQIRKNFAKSK---WRQA 308
QY 497 -----DASTSSCSEILPTSAEK 513
Db 309 FNATAVVRHMRKHLGSSLDSSNASVSSSLASQK 344

RESULT 15
US-10-936-445-4
; Sequence 4, Application US/10936445
; Publication No. US20050079530A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Greg
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Abuin, Alejandro
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Kinase Proteins and
; FILE REFERENCE: Polynucleotides Encoding the Same
; CURRENT APPLICATION NUMBER: US/10/936,445
; CURRENT FILING DATE: 2004-09-08
; PRIOR FILING DATE: US/10/446,175
; PRIOR FILING DATE: 2003-05-27
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-936-445-4

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; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-936-445-4

Query Match      22.2%; Score 603; DB 17; Length 356;
Best Local Similarity 38.1%; Pred.No.1.7e-36;
Matches 128; Conservative 62; Mismatches 106; Indels 40; Gaps 6;

QY 198 ICSGACGEVKLAFQKSVCKKAVAKIISKRKFKQNTSSNEHPISVDTEIEILKKLDHPCHII 257
Db 29 LGTGAFSEVVLAEERKATGKLFVAVKCIPIKKALKGES-----SIENEIAVLRKIKHENIV 82
QY 258 KIENFFDSEDFYIVLELMEGGELFDRVNVNSTRLEPIAKLYFYOMLLAVQYLHENGVIH 317
Db 83 ALEDIYESPNHLYLVNQLVSGGELFDRIVEKGFYTEKDASTLIRQVLDVAVYVLRMGIVH 142
QY 318 RDLKPNVLLSSTSECCIKITDFGOSKILGETSLMRTLCTGPTYLAPVLTAGTTGYS 377
Db 143 RDLKPNLHYYSODEESKIMISDFGLSKMEGRGDVNSTACGPGYVAPEVL---AQKPYS 199
QY 378 SAVDCWSLGVILFVCLCGYPPESEQNSNIPLNQIAEGKYTYIAAAWRNVSEQAFDLVKN 437
Db 200 KAVDCWSIGVIAYILLCGYPFPYDENDS-KLFEQILKAEYEFDSPWDDISDSAKDFIRN 258
QY 438 LLVVDPEQRLTTYKQALEHPWLQDDSMKHTVERLMYGVDPHTMPPPIKKNIIKRKGHEWDO- 496
Db 259 LMEKDPNKRYTCEQAAARHPWIAADTALNKNIH-----ESVSAQIRKNFAKSK---WRQA 308
QY 497 -----DASTSSCSEILPTSAEK 513
Db 309 FNATAVVRHMRKHLGSSLDSSNASVSSSLASOK 344
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Search completed: July 7, 2005, 13:06:39
Job time : 165 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 7, 2005, 12:50:39 ; Search time 43 Seconds
(without alignments)
897.525 Million cell updates/sec

Title: us-10-618-173-2

Perfect score: 2712

Sequence: 1 MMSRDTKTESQQSGTSSSS.....ASTSSCSEILPTSAEKRAKR 517

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/prodata1/iaa/5A COMB.pep.*
- 2: /cgn2_6/prodata1/iaa/5B COMB.pep.*
- 3: /cgn2_6/prodata1/iaa/6A COMB.pep.*
- 4: /cgn2_6/prodata1/iaa/6B COMB.pep.*
- 5: /cgn2_6/prodata1/iaa/6C COMB.pep.*
- 6: /cgn2_6/prodata1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2712	100.0	517	4	US-09-849-617-2
2	1655.5	61.0	543	4	US-09-529-093A-2
3	1655.5	61.0	543	4	US-09-529-154-2
4	1589.5	58.6	490	4	US-09-949-016-10788
5	603	22.2	356	4	US-09-733-388-4
6	603	22.2	356	4	US-10-446-175-4
7	600.5	22.1	355	4	US-09-579-664B-10
8	600.5	22.1	355	4	US-10-355-975A-10
9	600.5	22.1	385	4	US-09-733-388-2
10	600.5	22.1	385	4	US-10-446-175-2
11	591.5	21.8	370	2	US-08-878-796-19
12	591.5	21.8	370	3	US-09-272-796-19
13	591.5	21.8	370	3	US-09-457-040B-31
14	591.5	21.8	370	4	US-09-538-092-1314
15	591.5	21.8	415	4	US-09-949-016-7461
16	591.5	21.8	415	4	US-09-949-016-7462
17	580.5	21.4	476	4	US-09-960-643-2
18	575.5	21.2	776	1	US-08-198-446B-17
19	575.5	21.2	776	2	US-08-870-693-17
20	575.5	21.2	821	1	US-08-198-446B-6
21	575.5	21.2	821	2	US-08-870-693-6
22	559	20.6	513	4	US-08-248-796A-18515
23	531	19.6	473	4	US-09-538-092-1353
24	527	19.4	358	4	US-09-230-896C-29
25	525.5	19.4	456	1	US-08-464-164-2
26	525.5	19.4	456	1	US-08-338-057-2
27	525.5	19.4	456	2	US-08-668-416-2

28	517.5	19.1	817	4	US-09-992-481-4	Sequence 4, Appli
29	517.5	19.1	817	4	US-10-434-034-4	Sequence 4, Appli
30	501	18.5	765	4	US-09-975-326-4	Sequence 4, Appli
31	501	18.5	765	4	US-10-217-357-4	Sequence 4, Appli
32	501	18.5	766	4	US-09-975-326-2	Sequence 2, Appli
33	501	18.5	766	4	US-10-217-357-2	Sequence 2, Appli
34	496	18.3	729	4	US-09-949-016-6544	Sequence 6544, Ap
35	496	18.3	794	4	US-09-949-016-9883	Sequence 4, Appli
36	490	18.1	511	4	US-09-633-328B-4	Sequence 2, Appli
37	488	18.0	512	4	US-09-633-328B-2	Sequence 2, Appli
38	487.5	18.0	343	2	US-08-878-989-5	Sequence 5, Appli
39	487.5	18.0	343	3	US-09-272-796-5	Sequence 5, Appli
40	484.5	17.9	878	3	US-09-735-934A-2	Sequence 2, Appli
41	484.5	17.9	878	4	US-10-060-332-2	Sequence 2, Appli
42	484.5	17.9	878	4	US-10-339-657-2	Sequence 2, Appli
43	482.5	17.8	600	4	US-09-248-796A-18494	Sequence 18494, A
44	479.5	17.7	556	3	US-09-800-960-4	Sequence 4, Appli
45	479.5	17.7	556	4	US-10-096-960-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-09-849-617-2

; Sequence 2, Application US/09849617

; Patent No. 6593110

; GENERAL INFORMATION:

; APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY

; APPLICANT: GUO Zijian

; APPLICANT: DUNPHY, William

; TITLE OF INVENTION: CHECKPOINT-ACTIVATING OLIGONUCLEOTIDES

; FILE REFERENCE: CIT1350-1

; CURRENT APPLICATION NUMBER: US/09/849,617

; CURRENT FILING DATE: 2001-09-17

; PRIOR APPLICATION NUMBER: US 60/202,028

; PRIOR FILING DATE: 2000-05-04

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: Patent in version 3.0

; SEQ ID NO 2

; LENGTH: 517

; TYPE: PRT

; ORGANISM: Xenopus laevis

US-09-849-617-2

Query Match

Best Local Similarity 100.0%; Score 2712; DB 4; Length 517;

Matches 517; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMSRDTKTESQQSGTSSSSSSAPQSYSSQSSSSGTLSSLDTPVPQDLASIPEDPEIDED 60

Db 1 MMSRDTKTESQQSGTSSSSSSAPQSYSSQSSSSGTLSSLDTPVPQDLASIPEDPEIDED 60

QY 61 IPQPGRLWALGKGFNLHDLCLHEEYVFGDKKCDYDFIPVLNQTDRYKTSKRHFRIQ 120

Db 61 IPQPGRLWALGKGFNLHDLCLHEEYVFGDKKCDYDFIPVLNQTDRYKTSKRHFRIQ 120

QY 121 ELGHGHSRVANETDLSGNGTFVNKIIIGKRTLPLTNNAEIALSLPTNKVFVFSLSVDD 180

Db 121 ELGHGHSRVANETDLSGNGTFVNKIIIGKRTLPLTNNAEIALSLPTNKVFVFSLSVDD 180

QY 181 QTIYPKDFIDKYIMSRPIGSGACGEVKLAFQSKVCKKVAVKIISKRKFMONTSSNEHPTIS 240

Db 181 QTIYPKDFIDKYIMSRPIGSGACGEVKLAFQSKVCKKVAVKIISKRKFMONTSSNEHPTIS 240

QY 241 VDTTEILKLDHPICIIKIENFDSEDFYIIVLELMEGGELFDRVNVNSTRLEPIAKLYF 300

Db 241 VDTTEILKLDHPICIIKIENFDSEDFYIIVLELMEGGELFDRVNVNSTRLEPIAKLYF 300

QY 301 YQMLAVQYLHENGVIHRDLKPEENVLLSSTSECCIKITDFGSKTLGTSIMRTLCTGPF 360

Db 301 YQMLAVQYLHENGVIHRDLKPEENVLLSSTSECCIKITDFGSKTLGTSIMRTLCTGPF 360

QY 361 TYLAPEVLNTAGTGYSSAVDCWSLGVILFVCLGYPFSEQNSNIPLNQIAEGKYI 420
Db 361 TYLAPEVLNTAGTGYSSAVDCWSLGVILFVCLGYPFSEQNSNIPLNQIAEGKYI 420
QY 421 AAARNVSEQAFDLVKNLLVDPPEQLTTKQALEHPWLQDDSMKHTVERLMYGVDTHTMPP 480
Db 421 AAARNVSEQAFDLVKNLLVDPPEQLTTKQALEHPWLQDDSMKHTVERLMYGVDTHTMPP 480
QY 481 PIKKNIIIRKRGHEWDQDASTSSCEILPTSAEKRAK 517
Db 481 PIKKNIIIRKRGHEWDQDASTSSCEILPTSAEKRAK 517

RESULT 2
US-09-529-093A-2
; Sequence 2, Application US/09529093A
; Patent No. 6413755
; GENERAL INFORMATION:
; APPLICANT: LUYTEN, Walter H.M.L.
; APPLICANT: PARKER, Andrew E.
; APPLICANT: MCGOWAN, Clare H.
; APPLICANT: BLASINA, Alessandra
; TITLE OF INVENTION: Human Checkpoint Kinase, hCDS1, Compositions and Methods
; FILE REFERENCE: TSRI 649.0
; CURRENT APPLICATION NUMBER: US/09/529,093A
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: PCT/EP98/06981
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: GB 9722320.0
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 543
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-093A-2

Query Match 61.0%; Score 1655.5; DB 4; Length 543;
Best Local Similarity 59.9%; Pred. No. 98-152;
Matches 326; Conservative 74; Mismatches 105; Indels 39; Gaps 7;
QY 2 MSRDTKTESQ-----QSOGTSSSSSSSAP-QSYSQSSSSGTL 37
Db 1 MSRESDEVAQSHGSSACSPHGVSQTOSQSSSQSGISSTSTMPNSSQSSSSGTL 60
QY 38 SLDTPVPQDLASI-----PEDPEIDEDIPQWGRWLWALGKFLNHDCLHEBYVFGDKK 92
Db 61 SLETVSTQELYSIPEDQPEDEPEPTAPWRLWALQDGFANLECVDNDNYWFGDRKS 120
QY 93 CDYTFDIPVLNQTDRYKTSKRHFRIFOELGHGHSRVANIEDLSGNGTFFVNKEIIGKRT 152
Db 121 CEYCFDEPLLRKTDKRTYSKKHFRIFREVGPKNSYIAYIEDHSGNGTFFVNTLVGKGR 180
QY 153 LPLTNNAEIALSLPTNKVVFSDLSVDDOTIYPKDFIDKYIMSRPIGSGACGEVKLAFQK 212
Db 181 RPLNNSEIALSRNKNVVFDFLTVDQSVYPKALRDEYIMSKTLGSGACGEVKLAPER 240
QY 213 SVCKKVAVKIISKRFKMTSSNEHP-ISVDTEIELKLDHPICIIKENFFDSDFYI 271
Db 241 KTCCKVAIKIISKRFKAIGSAREADPALNVETEIELKLNHPICIIKNFFDAED-YI 299
QY 272 VLEMEGGLFDRVNVNSTRLEPIAKLYFYQMLLAVQYLHENGVIHRLDKPENVLSSSTS 331
Db 300 VLEMEGGLFDRVNVNSTRLEPIAKLYFYQMLLAVQYLHENGVIHRLDKPENVLSSSTS 331
QY 332 BECCIKITDFGSKILGETSLMRTLCTGPTTYLAPEVLNTAGTGYSSAVDCWSLGVILFV 391
Db 360 EDCLIKITDFGSKILGETSLMRTLCTGPTTYLAPEVLNTAGTGYSSAVDCWSLGVILFV 419
QY 392 CLCGYPPFSEQNSNIPLNQIAEGKYIYAAARNVSEQAFDLVKNLLVDPPEQLTTKQ 451
Db 420 CLSGYPPFSEHRTQVSKDQITSGKYNFIPVMAEVSEKALDVKLLVDPKARFTTEE 479
QY 452 ALEHPWLQDDSMKHTVERLMYGVDTHTMPP-----TKNIIIRKRGHEWDQDASTSS-----C 503
Db 480 ALRHPWLQDDSMKRFQDLLSEENESTALPQVLAQPSRKRPREGEAEGATTTKRPAVC 539

QY 452 ALEHPWLQDDSMKHTVERLMYGVDTHTMPP-----TKNIIIRKRGHEWDQDASTSS-----C 503
Db 480 ALRHPWLQDDSMKRFQDLLSEENESTALPQVLAQPSRKRPREGEAEGATTTKRPAVC 539
QY 504 SEIL 507
Db 540 AAVL 543

RESULT 3
US-09-529-154-2
; Sequence 2, Application US/09529154
; Patent No. 6531312
; GENERAL INFORMATION:
; APPLICANT: LUYTEN, Walter H.M.L.
; APPLICANT: PARKER, Andrew E.
; TITLE OF INVENTION: A NOVEL HUMAN CHECKPOINT KINASE, hCDS1, COMPOSITIONS
; FILE REFERENCE: JAB 1333 (US)
; CURRENT APPLICATION NUMBER: US/09/529,154
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: PCT/EP98/06982
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: GB 9722320.0
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 543
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-154-2

Query Match 61.0%; Score 1655.5; DB 4; Length 543;
Best Local Similarity 59.9%; Pred. No. 9e-152;
Matches 326; Conservative 74; Mismatches 105; Indels 39; Gaps 7;
QY 2 MSRDTKTESQ-----QSOGTSSSSSSSAP-QSYSQSSSSGTL 37
Db 1 MSRESDEVAQSHGSSACSPHGVSQTOSQSSSQSGISSTSTMPNSSQSSSSGTL 60
QY 38 SLDTPVPQDLASI-----PEDPEIDEDIPQWGRWLWALGKFLNHDCLHEBYVFGDKK 92
Db 61 SLETVSTQELYSIPEDQPEDEPEPTAPWRLWALQDGFANLECVDNDNYWFGDRKS 120
QY 93 CDYTFDIPVLNQTDRYKTSKRHFRIFOELGHGHSRVANIEDLSGNGTFFVNKEIIGKRT 152
Db 121 CEYCFDEPLLRKTDKRTYSKKHFRIFREVGPKNSYIAYIEDHSGNGTFFVNTLVGKGR 180
QY 153 LPLTNNAEIALSLPTNKVVFSDLSVDDOTIYPKDFIDKYIMSRPIGSGACGEVKLAFQK 212
Db 181 RPLNNSEIALSRNKNVVFDFLTVDQSVYPKALRDEYIMSKTLGSGACGEVKLAPER 240
QY 213 SVCKKVAVKIISKRFKMTSSNEHP-ISVDTEIELKLDHPICIIKENFFDSDFYI 271
Db 241 KTCCKVAIKIISKRFKAIGSAREADPALNVETEIELKLNHPICIIKNFFDAED-YI 299
QY 272 VLEMEGGLFDRVNVNSTRLEPIAKLYFYQMLLAVQYLHENGVIHRLDKPENVLSSSTS 331
Db 300 VLEMEGGLFDRVNVNSTRLEPIAKLYFYQMLLAVQYLHENGVIHRLDKPENVLSSSTS 331
QY 332 BECCIKITDFGSKILGETSLMRTLCTGPTTYLAPEVLNTAGTGYSSAVDCWSLGVILFV 391
Db 360 EDCLIKITDFGSKILGETSLMRTLCTGPTTYLAPEVLNTAGTGYSSAVDCWSLGVILFV 419
QY 392 CLCGYPPFSEQNSNIPLNQIAEGKYIYAAARNVSEQAFDLVKNLLVDPPEQLTTKQ 451
Db 420 CLSGYPPFSEHRTQVSKDQITSGKYNFIPVMAEVSEKALDVKLLVDPKARFTTEE 479
QY 452 ALEHPWLQDDSMKHTVERLMYGVDTHTMPP-----TKNIIIRKRGHEWDQDASTSS-----C 503
Db 480 ALRHPWLQDDSMKRFQDLLSEENESTALPQVLAQPSRKRPREGEAEGATTTKRPAVC 539

[illegible]


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/
/ REGISTRATION NUMBER: 36,749
/ REFERENCE/DOCKET NUMBER: PF-0321 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-855-0555
/ TELEFAX: 415-845-4166
/
/ INFORMATION FOR SEQ ID NO: 19:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 370 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: GenBank
/ CLONE: 790790
/
/ US-08-878-989-19
/
/ Query Match 21.8%; Score 591.5; DB 2; Length 370;
/ Best Local Similarity 39.9%; Pred. No. 1.1e-48;
/ Matches 124; Conservative 61; Mismatches 107; Indels 19; Gaps 5;
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/ QY 186 KDFIDKYMSPRIGSGACGEVKLAFQKSVCKKVAVKIISKRFKVMNTSSNEHPISVDTEI 245
/ Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
/ 14 EDIRDYDFRDVLGTGAFSEVLAEDKRTQKLVAIKCIAKEALGEGSGMEN-----EI 67
/
/ QY 246 EILKLDHPICIKIENFFDSEDFYIVLELMGEGELFDRVNVNSTRLRPIAKLYFYQMLL 305
/ Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
/ 68 AVLHKIKHPNIVALDDIYESGGHLIMQLVSGGELFDRIVEKGYTERDASRLIFQVLD 127
/
/ QY 306 AVQYLHENGVIHRDLKPNVLLSSSTSECCIKITDFGOSKILGETSLMRTLCGTPTYLAP 365
/ Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
/ 128 AVKYLHDLGIVHRDLKPNVLLSYLSDSKIMISDFGLSKMEDPGSVLSTACGTPGYVAP 187
/
/ QY 366 EVLNTAGTGYSSAVDCWSLGVILFVLCGYPFPSEQNSNIPLNQIAEGKYTIAAAWR 425
/ Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
/ 188 EYL---AQKPYSKAVDCWSIGVIAVILLCGYPFYDEN-DAKLFEQILKAIEYFDPSPYWD 243
/
/ QY 426 NVSEQAFDLVKNLLVVDPEQRLTTQKALEHPWLQDDSMKHTVERLMYGVDMTPPPIKKN 485
/ Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
/ 244 DISDSAKDFIRHLMKDPKFTCEQALQHPWIAGDT-----ALDKNIHQSVSEQIKKN 297
/
/ QY 486 IIRKRGHEWDQ 496
/ Db : : : : :
/ 298 FAKSK---WKQ 305
/
/ RESULT 12
/ US-09-272-796-19
/ Sequence 19, Application US/09272796
/ Patent No. 6207148
/ GENERAL INFORMATION:
/ APPLICANT: Bandman, Olga
/ APPLICANT: Hillman, Jennifer L.
/ APPLICANT: Corley, Neil C.
/ APPLICANT: Guegler, Karl G.
/ APPLICANT: Lal, Preeti
/ APPLICANT: Goli, Surya K.
/ APPLICANT: Shah, Purvi
/ TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
/ TITLE OF INVENTION: KINASES
/ NUMBER OF SEQUENCES: 21
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Incyte Pharmaceuticals, Inc.
/ STREET: 3174 Porter Drive
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
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/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/272,796
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/878,989
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J J
/ REGISTRATION NUMBER: 36,749
/ REFERENCE/DOCKET NUMBER: PF-0321 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-855-0555
/ TELEFAX: 415-845-4166
/ TELEX:
/
/ INFORMATION FOR SEQ ID NO: 19:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 370 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: GenBank
/ CLONE: 790790
/
/ US-09-272-796-19
/
/ Query Match 21.8%; Score 591.5; DB 3; Length 370;
/ Best Local Similarity 39.9%; Pred. No. 1.1e-48;
/ Matches 124; Conservative 61; Mismatches 107; Indels 19; Gaps 5;
/
/ QY 186 KDFIDKYMSPRIGSGACGEVKLAFQKSVCKKVAVKIISKRFKVMNTSSNEHPISVDTEI 245
/ Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
/ 14 EDIRDYDFRDVLGTGAFSEVLAEDKRTQKLVAIKCIAKEALGEGSGMEN-----EI 67
/
/ QY 246 EILKLDHPICIKIENFFDSEDFYIVLELMGEGELFDRVNVNSTRLRPIAKLYFYQMLL 305
/ Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
/ 68 AVLHKIKHPNIVALDDIYESGGHLIMQLVSGGELFDRIVEKGYTERDASRLIFQVLD 127
/
/ QY 306 AVQYLHENGVIHRDLKPNVLLSSSTSECCIKITDFGOSKILGETSLMRTLCGTPTYLAP 365
/ Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
/ 128 AVKYLHDLGIVHRDLKPNVLLSYLSDSKIMISDFGLSKMEDPGSVLSTACGTPGYVAP 187
/
/ QY 366 EVLNTAGTGYSSAVDCWSLGVILFVLCGYPFPSEQNSNIPLNQIAEGKYTIAAAWR 425
/ Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
/ 188 EYL---AQKPYSKAVDCWSIGVIAVILLCGYPFYDEN-DAKLFEQILKAIEYFDPSPYWD 243
/
/ QY 426 NVSEQAFDLVKNLLVVDPEQRLTTQKALEHPWLQDDSMKHTVERLMYGVDMTPPPIKKN 485
/ Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
/ 244 DISDSAKDFIRHLMKDPKFTCEQALQHPWIAGDT-----ALDKNIHQSVSEQIKKN 297
/
/ QY 486 IIRKRGHEWDQ 496
/ Db : : : : :
/ 298 FAKSK---WKQ 305
/
/ RESULT 13
/ US-09-457-040B-31
/ Sequence 31, Application US/09457040B
/ Patent No. 6387641
/ GENERAL INFORMATION:
/ APPLICANT: Vertex Pharmaceuticals Incorporated
/ APPLICANT: Bellon, Steve
/ TITLE OF INVENTION: Crystallized P38 Complexes
/ FILE REFERENCE: VPI/98-14
/ CURRENT APPLICATION NUMBER: US/09/457,040B
/ CURRENT FILING DATE: 1999-12-08
/ NUMBER OF SEQ ID NOS: 41
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 31
/ LENGTH: 370
/ TYPE: PRT
/ ORGANISM: Human
/
/ US-09-457-040B-31
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Query Match          21.8%; Score 591.5; DB 3; Length 370;
Best Local Similarity 39.9%; Pred.No.1.1e-48;
Matches 124; Conservative 61; Mismatches 107; Indels 19; Gaps 5;

QY      186 KDFIDKYIMSRPIGSGAGVEKLAFAQSVCKKVAVKIISKKEFKMNTSSNEHPISVDTEI 245
         :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db       14 EDIRDIYDFRDVLGTGAFFSEVILAEDRKTQLVAIKCAIKALGKGKGSMEN-----EI 67

QY      246 EILKKLDHPCIIKIENPFDSDFYYIVLELMEGGELEFDRVVNSTRLRREPIAKLYFYQMLL 305
         :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db       68 AVLHKIKHPNIVALDDIVESGGHLYLIMQLVSGGELFDRIVEKFYTERDASRLIFQVLD 127

QY      306 AVQYLHENGVIHRLDKBNVLLSTSECCIKITDFGOSKILGTSLMRTLCTPTYLAP 365
         :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db       128 AVKYLHLGIIVHRDLKPENLILYSLDEDSKIMISDFGLSKMEDPGSLVSTACGTFGVAP 187

QY      366 EVLNTACTTGYSSAADCWSLGVIPLFCVLCGYPPFESEQNSNIPLKNQAEGKYTVIAAAWR 425
         |||||----|||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db       188 EVL---AQKPYSKAVDCWSIGVIAYILLCGYPFPYDEN-DAKLEPQILKAIEYEDSPWD 243

QY      426 NVSEQAFLVKNLVLVDPEQRLLTKQALEHPWLQDDSMKHVTVERLMYGVDHTMPPIKKN 485
         :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db       244 DISDSAKDFIRHLMEXDKPEKRFTCEQALQHPWIAGDT-----ALDKNIHQSVSEQIKKN 297

QY      486 IIRKRGHEWDO 496
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Db       298 FAKSK--WKQ 305

RESULT 14
US-09-538-092-1314
; Sequence 1314, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Glot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurapatSeqFormatter Version 0.9
; SEQ ID NO 1314
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Polypeptide Accession Number Q14012
US-09-538-092-1314

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	Query Match	21.8%	Score 591.5	DB 4	Length 370
	Best Local Similarity	39.9%	Pred. No. 1.1e-48		
	Matches 124	Conservative 61	Mismatches 107	Indels 19	Gaps 5
Qy	186	KDFIDKYIMRSPIGSGACGEVKLAFQKSVCKKAVKIISKRFKXMTSSNEHPISVDTEI	245		
Db	14	EDIRDIYDFRDVLGTGAFSEVILAEEDKRTQKLVAIKCIAKEALGKEGSMEN-----EI	67		
Qy	246	EILKKLDHPICIIKIETNPFDSDFYIIVLELMEGGELFDRVNVNSTRLRPIAKLYFYQMLL	305		
Db	68	AVLHKIRKPNIVALDDIYESGGHYLLIMQLVSGGELFDRIYVEKGFYTERDASRLIFQVLD	127		
Qy	306	AVQYLHENGVIHRLKDPENVLLSTSBECCTKIITDPGQSKILGETSLMRTICGGPTTYIAP	365		
Db	128	AVKYLHDLGIYHRLKDPENLLYVSLDEDSKIMISDFGLSKMEDPGLVSTACGPGFYVAP	187		

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366 EVLNTAGTTCYSAVDCWSJGVILFVCLCGYPPPPSEONSIPLKNQTAEGKTYTIAAAWR 425
188 EVL---AQPKYSKAVDCWSJGVIAIYILLCGYPPPYDEN-DAKLFEQILKAEYEFDSPYWD 243
426 NVSEQAFDLVKNLLVDPQORLTTKQALEHPWLQDDSMKHTVERLMYGVHDHTMPPPIKKN 485
244 DISDSAKDFIRHLMEKDPKRKFTCEQALQHPWIAGDT-----ALDKNIHOSVSEQIKKN 297
486 IIRKRGHEWDQ 496
298 FAKSK---WKQ 305

RESULT 15
US-09-949-016-7461
; Sequence 7461, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 7461
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7461

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Query Match	21.8%	Score	591.5	DB	4	Length	415
Best Local Similarity	39.9%	Pred. No.	1.3e-48				
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Gaps	5						
Qy	186	KDFIDKXIMSRPTGSGACGKVLAFOKSVCKKVAVKLIISKRFKPMWTSSEHHPISVDEI	245				
Db	59	EDIRDIYDFRDVLGTGAFSVILAEADRKTQKLVAIKCAKEALGKGGSMEN-----EI	112				
Qy	246	EILKLDHPICIIKIENPFDSDEFYIVLELMEGEGLFDRVNVNSTRLEPIAKLYFYQWLL	305				
Db	113	AVLHKIKHPNIVALDDIYESGGHYLIIMQLVSGGELEFDRIVEKGFYTERDASRLIFQVLD	172				
Qy	306	AVQYLHENGVIHRDLKPENVLLSTSECCIKITDFGQSKILGETSLMRTLTCGTPTYLAP	365				
Db	173	AVKYLHDLGIVHRDLKPENLYYSLDBDSKIMISDFGLSRMEDPGSVLSTACGTPGVVAP	232				
Qy	366	EVLNTAGTTGTYSSAVDCWSGVILFVCLCGYPPESEONSNIPLKNOIAEGKYTYIAAAWR	425				
Db	233	EVLI---AQPYSKAVDCWSGVITAYILLCGYPFPYDEN-DAKLFEQILKABYEEDSPYMD	288				
Qy	426	NVSEQAFDLVKNLVVDPEORLTTKQALEHPWLOQDSSMKHTVERLMYGVDHMTPPPIKKN	485				
Db	289	DISDSAKDFIRHLMWKDPEKRFTCEQALQHPWTAGDT-----ALDKNIHQSVSEQIKKN	342				
Qy	486	IIRKRGHEWDQ	496				
Db	343	FAKSK---WKQ	350				

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Job time : 44 secs

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